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is the number of results predicted by chance to have a
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Copyright (c) 1993 - 2003 Compugen Ltd.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Query Match 100.0%; Score 2388; DB 6; Length 2389; Best Local Similarity 100.0%; Pred. No. 0; Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATGGTGTTTCCTA 60	Fannon,M.R. and Rosen,C.A. Streptococcus pneumoniae antigens and vaccines Patent: US 6159469-A 55 12-DEC-2000; Location/Qualifiers 1. 2389 2e	.1 GI:14103841 iled. ; 1 to 2389) ; Kunsch.C.A Barash.S.C Dillon.P.J	RESULT 1 AR120265 LOCUS AR120265 2389 bp DNA linear PAT 16-MAY-2001 DEFINITION Sequence 55 from patent US 6159469.	ALIGNMENTS	57.2 2.4 250421 3 AE014849 AE014849 57 2.4 84618 5 AL591365 AL591365 57 2.4 203138 2 BX530070 BX530070 56.4 2.4 151343 5 AL929536 AL929536	94 57.2 2.4 110000 2 PFMALBEL 02 95 57.2 2.4 114226 2 AC004710 96 57.2 2.4 116426 2 AC005507 96 57.2 2.4 156490 2 AC005507	58.2 2.4 25234 3 AE014833 AE029250 5 AL929250 5 AL929250 AE0214840 5 AE014840 5 AE014840 AE014840 5 AE014840 AE	85 60 2. 86 59.4 2. 88 58.6 2.	60.4 2.5 213924 3 AE014822 AE014822 60.2 2.5 51999 9 AC099341 AC099341 60.2 2.5 213544 2 BX510939 BX510939	76 61.4 2.6 250195 3 AR014831 AR014831 78 61.4 2.6 250195 3 AR014831 AR014831 AR014831 79 60.6 2.5 96249 9 AC116612 AC116612 AC116612 BX537105 GC COLLEGE COLL	64 2.7 14337 9 AC100791 AC100791 63.4 2.7 170523 9 AP002387 AP002387	70.6 3.0 115758 9 AC104634 AC104634 Homo it and it	102.6 4.3 1239 6 75.6 3.2 110000 2 75.6 3.2 198550 2 75.4 3.2 110000 2
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PC G01N33
CC Strand
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Kunsch,C.A., Choi,G.H., Johnson,S.L. and Hromockyj,A.
Streptococcus pneumoniae antigens and vaccines
Patent: JP 2001505415-A 28 24-APR-2001;
HUMAN GENOME SCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BD063274 2389 bp DNA Streptococcus pneumoniae antigens and vBD063274 GI:22608877 JP 2001.505415.ed unidentified unidentified
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R 31-OCT-1996 US 60/029960

I CHARLES A KUNSCH,GIL H CHOI,SYDNOR L JOHNSON,ALEX HROMOCKYJ PC C12N15/31,C12N5/18,C12N1/21,C07K14/315,C12Q1/68,A61K39/09, PC
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Streptococcus.	1441 TAAAGAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCCAATTACCCATCCAGAGCG 1500	B
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ر در د	661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720	B 68
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QY 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900	QY 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840	OY 721 TGTAAGCAATCCAGGAACTACAAATACTAACAGCAAGCAA	QY 661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720	QY 601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660	QY 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600	QY 481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540	Qy 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480	OY 361 TGCCCACGCGGATAACGTCCGTACAAAAAGAGGAAATCAATC	OY 301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360	OY 241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300	OY 181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240	OY 121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180	OY 61 TATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120	QY 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTTCCTA 60	Query Match 100.0%; Score 2388; DB 6; Length 2406; Best Local Similarity 100.0%; Pred. No. 0; Matches 2388; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	/mol_type="genomic DNA" /mol_t	Patent: Work Sp. Chiron Sp. 128	TITLE Streptococcus pneumoniae proteins and nucleic acids
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(phtA) gene, co
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AF291695.1 GI
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Submitted (01-AUG-2000) Molecular Biology, Human Ge
Inc., 9410 Key West Ave., Rockville, MD 20850, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                     Wizemann, T.M., Heinrichs, J.H., Adamou, J.E., Erwin, A.L., Kunsch, C., Choi, G.H., Barash, S.C., Rosen, C.A., Masure, H.R., Tuomanen, E., Gayle, A., Brewah, Y.A., Walsh, W., Barren, P., Lathigra, R., Hanson, M., Langermann, S., Johnson, S. and Koenig, S. Use of a whole genome approach to identify vaccine molecules affording protection against Streptococcus pneumoniae infection Infect. Immun. 69 (3), 1593-1598 (2001)
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Best Local Similarity Matches 2389; Conserv TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTTCCTA ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180 TATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAACCTGGGTACCTTC ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACCATTCCTAAGAATGAGTT TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTTGGCACGTTCGCA GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAAATACTATGTTTACCTTAAGGATGC TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA TTCACATGGCGACCACTATCATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC TATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG Conservative 100.0%; 0; Score 2388; Pred. No. 0; Mismatches DΒ 1; 0; Indels Length 0 Gaps 600 540 629 480 420 449 209 60 780 869 720 809 749 689 569 509 389 329 0

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2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTAG		1.TGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAGACCACAGTGAAGATCCAAA		9 1-31-3		1741 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTA 1800 	1681 CCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 1740 	1621 TGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG 1680 	1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1620 	1501 ACTIGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT 1560 	1441 TAAAGAAAATTGGTAGATGATTTATTGGCATCCTAGCACCAATTACCCATCCAGAGCG 1500 	1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 1440 	1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380 	1261 TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320

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AE007418 Streptococcus genome AE007418 AE005 AE007418.1 GI	TGACTC	TAACGGAT	AAGTAGAG AAGTAGAG	AGAACTTC	GATGGGGC GATGGGGC	TGTTTGCG	AATTTGCT	CAGTTGAG	ATCGTGTG ATCGTGTG	CATCTCCA	TTTCTGAT	BAAGGAGAT BAAGGAGAT	CTGATAAG CTGATAAG	TTGGCAAA TTGGCAAA	HIIIIIII VAAGAAAAA
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10256 ae TIGR 9 9	GATAACAATCT	AAAGCCAAI	GTAGAAGCO	GAAGAGCC <i>I</i> 	GAGCATGTO	TACTACGTA	GATCACACI GATCACACI	GGTAATTTC	AAACGAATT AAACGAATT	GTTAAAGC! GTTAAAGC!	GTTGCAGCT	ACGCCTCAI	TCAGATGGI	CAAATTGAC	GATTTATTO
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31-AUG-2001 He complete	ACTTGC 539	NAATAA 2280 NAATAA 5332 NCTTGC 2340		AGTCCC 2160	TCCAAA 2100 CCAAA 5152	TAATGA 2040 AATGA 5092	GGAAGA 1980 GAAGA 5032	TAATAT 1920 AATAT 4972	TGAGCA 1860 TGAGCA 4912	TATTTA 1800	CCTACC 1740 CCTACC 4792	AGATAG 1680 AGATAG 4732	CAGTGA 1620 CAGTGA 4672	TCAATT 1560	 AGAGCG 4552
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SdD

Sg gene

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DNGFGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKPEEETPREEKPQSEKPESPKPT
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SHNHNSRADNAVAAARAQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNEL
SASELAAAAAYWNGKQGSRPSSSSSYNANPAQPRLSENHNLTVTPTYHQNQGENISSL
LRELYAKPLSERHVESDGLIFDPAQITSRTARGVAVPHGNHYHFIPYEQMSELEKRIA
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complement (8049.
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                                                                                                                                                                                  HSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKEA
EVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to GP:4249624; identified by sequence
similarity; putative"
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/gene="SP1175"
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QDNNTIMAEAEKLLALLKESK"
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/gene="SP1174"
/hote="similar to GP:4249624; identified by sequence
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complement(2729. .5188)
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complement(1933. .2307)
                                                                                                          complement (8049. .9782)
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                                                                        /gene="SP1176"
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/protein_id="AAK75282.1"
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   TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT
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TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG
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                                                                                                                                                                                                                    TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCCTTGGCACGTTCGCA
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TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACCATTCCTAAGAATGAGTT
                                                                                                                              AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC
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llarity 100.0%;
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a 2089 c 1850 g 3475 t
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TMDIGGDKELPYFDMPHEMNPPLGFRALRISISETGDAMFRTQIRALLRASVHGQLRI
MFPMVALLKEFRAAKAVFDEEKANLLAEGVAVADNIQVGIMIEIPAAMAMLADQFAKEV
DFFSIGTNDLIQYTMAADRMNEQVSYLYQPYNPSILALINNVIKAAHAEGKWAÇMCGE
MAGDQQAVPLLVGMGLDEFSMSATSVLRTRSLMKKLDTAKMEEYANRALTECSTMEEV
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IAHDLTPSDTAQLDKNFVKAFVTNIGGRTSHSAIMARTLEIAAVLGTNNITEIVKDGD
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REFERENCE AUTHORS TITLE JOURNAL FEATURES SOUIC	RESULT 8 AX571763/c LOCUS DEFINITION ACCESSION VERSION VERSUN KEYWORDS SOURCE ORGANISM	д Q У	db Qy	Db Qy	dg Qy	Qy	Db Qy	DB Qy	D Qy	Qy da	Qy Db	Db db	dy Qy
Streptococcus Streptococcus 1 Masignani, V., Tettelir Streptococcus pneumoni Patent: WO 02077021-A Chiron Spa (IT); THE Location/Qual Location/Qual 1. 349980 /organism="St /mol_type="g /db_xref="tax /note="seq 45 following sec 4980: from 0.	AX571763 Sequence 4982 from Patent WOO2077021. AX571763 AX571763.1 GI:26003955 Streptococcus pneumoniae Streptococcus pneumoniae Streptococcus pneumoniae	2341 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAATAAAC 2389 	2281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC 2340 	221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA 2 	2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGC	2101 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC 2160	2041 TGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGA	1981 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATGA 2040	1921 TAAATTIGCTIGGITIGATGATCACACATACAAAGCTCCAAAIGGCTATACCTIGGAAGA 1980 	1861 TACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAATAT 1920 	1801 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1860 	1741 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTA 1800 	1681 CCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 1740

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/strain="R6" /db_xref="taxon:171101" complement(91738) /gene="spr1056"	source 110320 /organism="Streptococcus pneumoniae R6" /mol_type="genomic DNA"	Company, Lilly Research Labs, Indianapolis, IN 46285-0438, USA Location/Qualifiers	and Glass, J. I. Direct Submission	Sun, PM., Winkler, M. E., Yang, Y., Young-Bellido, M., Zhao, G., Zook, C., Baltz, R. H., Jaskunas, S. R., Rosteck, P. R. Jr., Skatrud, P.L.	McLeaster, K., Mundy, C., McLeaster, K., Mundy, C.,	Jenoli, B.S., Estrem, S., Filiz, L., FulpJ., Fuller, W., Gerlinger, C., Gilmour, R., Glass, J.S., Hann, A., Khoja, H., Kratt, A., LaGace, R., Ioblaco J. Tool N. Tofrovitz P. T. T. Mateurahima D.	2 (bases 1 to 10320) 2 (bases 1 to 10320) 3 (bases 1 to 10320) 4 (bases 1 to 10320) 5 (bases 1 to 10320) 5 (bases 1 to 10320) 6 (bases 1 to 10320) 7 (bases			Sun, PM., Winkler, M.E., Yang, Y., Young-Bellido, M., Zhao, G., Zook, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L.	McAhren,S., McHenney,M., McLeaster,K., Mundy,C., Nicas,T.I., Norris,F.H., O'Gara,M., Peery,R., Robertson,G.T., Rockey,P.,	Khoja,H., Kraft,A., LaGace,R. Lefkowitz,E.J., Lu,J., Matsus			Streptococcus pneumoniae R6	N AE008479 AE007317 AE008479.1 GI:15458677	Streptococcus pneumoniae R6 section 95 of 184 of the complete genome.	AE008479 10320 bp DNA	2341 GIIGIIAAAAGAAAIAAICCIICAICIIGIAAGAAGAAAAAAAA	TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAA	TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAATTACTTGC	104730 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA 104671	2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA 2280	2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGC		TGGATGGGGCAATGCCAGTGAGCATGTTTAGGCAAGAAAGA	
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KEEINRQKQEHSQHREGGTPRNDGAVALKSQGRYTTDGJIRVDGKYYVYLKDAAHADNVRT
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PHGHYYY PKNELEASELAAAEAFLSGRGNISNSRTYVRRQNSDNTSRTIMVPSVSNP
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GVAVPHGDHYHFIPYSQMSELEERIARIIPLEKKRSHHWPDSRPEGPSPOPTPEPSPG
PQPAPNLKIDSNSSLVSQLVRKVGGEYVFEEKGISRYVFAKDLPSETUKNLESKLSKQ
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PVEETPAEPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTIQIM
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/tzanslation="MASKDEHVVAETGIHARPATLLVQTASKFASDITLEYKGKSVNL
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                                                                                                                                                                                                                                                                                                                                      /note="synonym: spr1063"
complement(9861. .10124)
/gene="ptsH"
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DFFSIGTNDLIQYTMAADRMNEQVSYLYQPYNPSILRLINNVIKAAHAEGKWAGMCGE
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/translation="MTEMLKGIAASDGVAVAKAYLLVQPDLSFETITVEDTNAEEARL
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complement(8122. .9855)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="synonym: spr1062" complement(8122. .9855)
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complement(5417. .7903)
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NEEKPQTEKPEEETPREEKPQSEKPESPKPTEEPEEESPEESPEESEEPQVETEKVKE
                                                                                                                                                                        the PTS"
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IAHDLTPSDTAQLDKNFVKAFVTNIGGRTSHSAIMARTIBIAVLGTNNITEIVKDGD
ILAVNGITGEVIINPTDEQAAEFKAAGEAYAKOKAEWALLKDAOTVTADGKHFBLAAN
IGTPKDVEGVNNNGAEAVGLYRTEFLYMDSQDFPTEDEQYEAYKAVLEGMNGKPVVVR
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                                                                                                                                                                                             /label=5pr1063
/product="Histidine-containing phosphocarrier protein
                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=11
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/db_xref="GI:15458683"
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960 6849	901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT	Qy	
900	841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC	Qy Db 6	
840 6969	781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG	Qy Db 7	
780 7029	721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAACAGCAACACCTAACAGTCA	Qy Db	
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660 7149	601 ATCAGCTAGCGAGTTGGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA	Qy Db 7	
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120 7689	61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA	Qy 55	
60 7749	1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA	Qy Db 7	
0;	tch 99.0%; Score 2365.6; DB 1; Length 10320; al Similarity 99.4%; Pred. No. 0; 2374; Conservative 0; Mismatches 15; Indels 0; Gaps	Query Mat Best Loca Matches	
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Submitted (31-OCT-2000) Research Department,
Severo Ochoa 2, 28760 Tres Cantos, SPAIN
* NOTE: This is a "working draft' sequence.
* This sequence will be replaced
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	/ Match 60.0%; Score 1434.4; DB 1; Local Similarity 79.0%; Pred. No. 5.1e-296; Les 1724; Conservative 0: Mismarches 447; I	EETPREEKPQSEKPESPKPTEEPEEESPEESPEESPEERVKEKLREAEDLLGK IQNPIIKSNAKETLTGLKUNLLFGTQDNNTIMAEAEKLLALLKESK" BASE COUNT 880 a 518 c 533 g 604 t ORTGIN	VDDILAFLAPIRHPERLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEG DAYVTEHMTHSHHIKKDSLSEJAFAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIY NRVKAAKKVELDEMPFYNLOYTVEVKNGSLIIPHYDHYNNIKFEBFDEGLYEAPKGYSL EDLLATVKYYVEHPNRRPHSNAGFGNASOHVONGKOADTNOTEKPE EDLLATVKYYVEHPNRRPHSNAGFGNASOHVONGKOADTNOTEKPE	TNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLIFDPAQITSRTANGVAVPHGDHYHF IPYSQLSPLEEKLARIIFDRANGWYPDSRFEQDFSPQSTEBSSFSPQBAPNDQBAFS NPIDEKLVKEAVRKVGDGYVFEENGVPRYIPAKDLSAETAAGIDSKLAKQESLSHKG AKKTDLPSSDREFYNKAYDLARIHODLLDNKGROVDFEALDNLLEERLKDVSSDKVKL	QATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISEE LLMKDBNYQLKDEDIISEIKGGYVIKVDGKYYVYLKDAAHADNNETKEEINROKQEHS QHREGGTPRNDGAVALARSQGRYTTDDGYIFNAADIIIEDTGDAYIVPHGDHYHYIPK ELSAAELAAAKFLSGRGNLSNSRTYRBONSDNYSRTNWYPSVGNEGTYNTNTSNNSN	/product="PhpA" /protein_id="AAK26629.1" /db_xref="GI:13447094" /translation="MKINKKYLVGSAAALILSVCSYELGLYOARTVKENNRVSYIDGK	/gene="hhpA" /note="histidine motif-containing protein" /codon_start=1 /trans1_table=11	1	/db _ref="taxon:1313" dene 1. 2535	/mo] type="denomic DNA"	foc	TITLE Direct Submission JOURNAL Submitted (25-JAN-2001) Department of Bacter: JOURNAL Vaccines 211 Bailey Doad West Honrists N		MEDILINE 21246685 PUBMED 11349048	Recombinant PhpA protein, a protein from Streptococcus i intranasal pneumococcal chainfect tmmin 60 (6) 3827.	REFERENCE 1 (bases 1 to 2535) AUTHORS Zhang,Y., Masi,A.W., Barniak,V., Mountzouros,K., Green,B.A.	Streptococcus pneumoniae Bacteria; Firmicutes; Lactobacillales; Streptococcus.	Streptococcu	AF340221 2535 bp DNA Streptococcus pneumoniae PhpA (phpA) gene, AF340221 1 GT:13447093	RESULT 11	Qy 2340 CGTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAAATAAAC	OY 2280 ATTIGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAATTACTTG
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CCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGT 1128	GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080 	GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020 	AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960	TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900 	AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840 	TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780 	TTCANGAACCTATCGCCGACAAATAGCGATAACACTTCAAGAACAACTGGGTACCTTC 720		ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660	TGGTGATGCTTATATCGTTCCTCACGGCGACCATTACCATTACATTCCTAAGAATGAGTT 659	ATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600	GGGACGCTACACCACAGATGATGGTTATATCTTTAATGCTTCTGATATCATTGAAGATAC 599	COMPARAGETGGGACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCACA 539	8	TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC	ANTCANGGGTGGTATGTGATTANGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 419	HATTGCTGATGAAGGATCCAAACTACCAGCTAAAGGACGAGGATATTATCAGTGA 359	TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300	TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240	GCGTGAAGGAATCAATGCTGACGAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180 		TATAGATGGA BABAGA GCGA GGCA BABABAGGGA BATTTGA CTCCTGATGA TGAGGTTA CCABA 120

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SHIRE BIOCHEM INC. (CA)
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AX343073 Sequence 4 from I AX343073 AX343073.1 GI:18 unidentified unidentified unclassified. Hamel,J., Ouellet,C., Charland,N., Streptococcus antigens Patent: WO 0198334-A 4 27-DEC-2001; SHIRE BIOCHEM INC. (CA) 934 1. .2647 /note="BVH-11" 538 c 55 /organism="unidentified'
/mol_type="genomic DNA"
/db_xref="taxon:32644" Location/Qualifiers GI:18152271 2647 bp Patent WO0198334 556 Ω 619 Martin, D. ct DNA linear and Brodeur, PAT 12-JAN-2002

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CCCTTCGTTATC	ACCACTTCATCC	CTTGTCTTTGATCCAGCACAAATCACAAGT	CTTGAAACAGCTCTACAAAC	\GCAACAACAGCAACACT. \GCAACAACAGCAACACT.	AGCGATAÁCACTTCAAGAACAAACT 	CTTCCTATCTGGTCGAGGAAATCTG	CCATTACATTC	ATGCTTC	TGCTGTTG	ATCAATCGACAAA ATCAATCGGCAAAA	AAATACTATGTTTA AAATACTATGTTTA	CAAACTATAAGCTAAAAGATGAGGATA 	AATGGTAAGGTTCCTTATG! 	CAAGATAACAGACCAA CAAGATTACGGATCAA	GACTCCT	aacggttaaggaaaataat aactgtaaaagaaaataat	DB 6; Length -283; 539; Indels
CAAACCATTG CAAACCATTG	CTTACTCTCAAAT TATGAACAAAT	CGAAC	TGCCTTTGAG TGCCTTTGAG	AACAGTCA AACAGTCA	CTGGGTACCTTC CTGGGTACCTTC	TCAAA	CTAAGAATGAGTT CTAAGAATGAGTT	TGATATCATAGAGGATAC	CCTTGGCACGTTCGCA	CAAGAGCATAG CAAGAACATAG	8-8	TTGTTAATGA TTGTCAATGA	CTTATGACGCTATCATCAG 	GGCTATGTCAC GGTTATGTGAC	GATGAGGTTAGCAA GATGAGGTTAGCAA	CGTGTTTCCTA CGTGTTTCCTA	102; Gaps
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300 CAGTGAAGAGCTCCTCATGAAAGATCCGAATTATCAGTTGAAAGGATTCAGACATTGTCAA 359 298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357	38 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAAGATGAGGATATTGTTAA	178 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237	118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177	58 CTATATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG 117	TCTTACGAGTTGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGT 	Watch 41.6%; Score 993; DB 6; Length 2457; Local Similarity 65.8%; Pred. No. 1.1e-201; nes 1611; Conservative 0; Mismatches 696; Indels 141; Gaps 6;	/mol_type="genomic DNA" /db_xref="taxon:1313" 836 a 497 c 531 g 593 t	Chiron Sp	1 Masigna Strepto Patent	Streptococcus pneumoniae SM Streptococcus pneumoniae Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.	Sequence 2345 from Patent AX569137 AX569137.1 GI:26002635	AX569137	2299 GGATAACAATAGTATCATGGCAGAAGCAGAAAATTACTTGCGTTGTTAAAAGGAAGTAA 2358	2239 GAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAATTTGACTCTTCAAATTAT 2298	2179 AGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAAAGTAACGGATTCTAGTCT 2238	2126CCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGAAAA 2178	2264 GGAAGAAACCCCTCGAGAAGAAAACCACAAAGCGAGAAACCAGAGTCTCCAAAAACCAAC 2323	2126 2125	
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misc_feature	2409 TATTATGGCAGAAGCTGAAAAACTATTGGCTTTATTAAAGGAGAGTAA 2456	Дb
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TITLE Direct (JOURNAL Submitte West Was	1738 ACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTAT 1797	Db Qy
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TITLE Identif pneumoco JOURNAL Infect. MEDIINE 211010A	1618 TGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGA 1677	Db Qy
REFERENCE 1 (base AUTHORS Adamou, Dormitze	1558 ATTAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAG 1617 	p Q
SOURCE Strepton ORGANISM Strepton Bacteria	1498 GCGACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAAGACGAAGTTCGTATTGCTCA 1557	ДУ
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                                                                                                                 Submitted (03-NOV-2000) Molecular Microbiology, West Watkins Mill Road, Gaithersburg, MD 20878, Location/Qualifiers
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AF318955
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                                                                                                                                                                 Direct Submission
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TGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTT
                            GGCCAAGCAGGAAAGTTTATCTCATAAGCTAGGAGCTAAGAAAACTGACCTCCCATCTAG
                                                      ATCAAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAAAAAAGAAAATGTTGCTCCTCG
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REFERENCE
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                                          Streptococcus pneumoniae
Streptococcus pneumoniae
Bacteria; Firmicutes; Lactobacillales;
Masignani,V.,
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838 GAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCG 897	778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 837	718 TTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACCTAACAG 777	658 AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717	598 GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 657	538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597	478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537	418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCCTTTGGCACGTTC 477	358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC	298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357	238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA 297	178 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237	118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177	58 CTATATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG 117	1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTC 57	/ Match 41.4%; Score 990; DB 6; Length 2517; Local Similarity 68.1%; Pred. No. 4.7e-201; les 1478; Conservative 0; Mismatches 636; Indels 57; Gaps 5;	/mol_type="genomic DNA" /db_xref="taxon:1313" 830 a 509 c 545 g 633	Chiron Space	
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9561156	/gene="SP0996" /note="This region contains a match to at least one other /note="This region contains a match to at least one other gene that is not full length, and is not the result of a sequencing artifact; similar to GP:5019553; identified by sequence similarity; putative; IS630-Spn1, transposase	/gene="SP0995" 655795	/db_xref="taxon:170187" 129476	/organism="Streptococcus pneumoniae TIGR4" /mol_type="genomic DNA" /mol_type="genomic DNA"	Qualifiers	Direct Submission Submitted (29-JUN-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Bockville MD 20850 USA	.J., Ujwal,M.L., Yang,F., Smith,H.O., Venter,J.C., y,B.A., Morrison,D.A., Hollingshead,S.K. and Fraser,C.M.	m,T.V., Angiuoli,S., Gesuwan,P., Hickey,E.K., Holt,I.E.,	.B. LO LIDGL, K.E., Paulsen, I.T., Eisen, J.A., Read, T.D., (1988), R.G., Heidelberg, J., DeBoy, R.T., Haft, D.H., Dodson, R.J.,		genome sequence of a virulent isolate of Streptococcus ae 203 (5520) 400 506 (2001)		le.E., Khouri, H., Wolf, A.M., Utterback, T.R., Hansen, C.L., L.A., Feldblyum, T.V., Angiuoli, S., Dickinson, T., K.K., Holt, I.E., Loftus, B.J., Yang, F., Smith, H.O., C. Doubhertv B.A. Morrison D.A., Hollingshead S.K. and	eidelberg,J., DeBoy,R.T., Haft,D.H., I winn,M., Kolonay,J.F., Nelson,W.C., Pe hito Callary I I I Po	11931) elson,K.E., Paulsen,I.T., Eisen,J.A.	occus pneumoniae TIGR4	:14972469	ABO05672	Occurs presumpnias TTGPA section RE of 194 of the complete	TGATG 2188	AGAAG 2156	CAGTGAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGC 2145	TCCACATTCTAATGATGGATGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGA	CTATACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACG 2025
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DSPSAQRYSESDGLVEDDAKI I SRTPNGVA I PHODHYHF I PYSKLSALEEKI ARMVPI
SGTGSTVSTNAKENEVVSSLGSLSSNPSSLTTSKELSSASDGY I FNPKDI I VEETATAY
I VRHGDHFHY I PKSNQ I QQPTL PNNSLATPS PSILP I NPGTSHEKHEEDGYGFDANRI I I
AEDESGFVMSHGDHNHY FFKKDLITEGQ I KAAQKHLEEVKTSHNGLDSLSSHEQDYPSN
AKEMKDLDKKI EEKI AGI MKQYGYKRESI VVNKEKNAL II Y PHOHHHADPI DEHKPVG
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VKDNEKVNSNYAVARSQGRYTTNDGYVFNPADIIEDTGNAYIVHGGHYHYIFKSDLS
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8670. .11789
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PERLGKRNAQ I I YTDDE I QVAKLAGK YITEDGY I FDROI TSDEGDA YVTPHMTISHW
I KKOSLSEA ERAAQAYAKEKGLTPEGTTHODSGNTEAKHABAT YNR VKAAKKYELDE
MPYNLQYTVEVKNGSL I I PHYDHYHNI KPEWFDEGLYBAPKGYTLEDLLATVKYYVEH
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SHNHGGGSNDQAVVAARAQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNE
LSASELAAAEAYWNGKQGSRPSSSSSYNANPAQPRLSENHNLTVTPTYHQNQGENISS
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VKEVSGDLNDVRMIQSSGGIHSTEPSANDIARITAM
KEVSGDLNDVRMIQSSGGIHSTEPSANDIARITAM
KESKYKVLEASEGMTLERVPGLEDVEADGVDEKTLVDPWYHMLDPEKAGEEAQIIAKRFGLN
SEVDSEHKETYQKNAQAFIKKAQELTKKRQPKFEKATQKTFVTQHTAFSYLAKRFGLN
OLGIAGISPEQEPSPRQLTEIQEFVKTYKVKTIFTESNASSKVAETLVKSTGVGLKTL
QLGIAGISPEQEPSPRQLTEIQEFVKTYKVKTIFTESNASSKVAETLVKSTGVGLKTL
                                                                                                                                                        VRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYI
VEVPILEKENQTDKPSILPQFKRNKAQENLKLDEKVEEPKTSEKVEKEKLSETGNSTS
NSTLEEVPTVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLPSGEVIKKNMADFTG
                                                                                           EAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKPENSTDNGMLNPE
GNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTIELRLPSGEVI
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ADNLYKPSTDTEETEEAEDTTDEAEIPQVENSVINAKIADAEALLEKVTDPSIRQNA
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DQAGQKAENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISE
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5941. .8460
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/product="conserved hypothetical
/product="AAK75121.1"
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/protein_id="AAK75119."
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Matches 1478;
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Local Similarity
1018 TTGGGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCC 1077
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                                                                              AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCCTTCGTTATCGTTCAAACCA
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Pred. No. 4.6e-201
0; Mismatches 636
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Dopazo, J., Mendoza, A., Herrero, J., Caldara, F., Polissi, A.,
Humbert, Y., Friedli, L., Guerrier, M., Grand-Schenk, E., Gandin, C.,
Francesco, M., Buell, G., Feger, G., Garcia, E., Peitsch, M. and
Garcia-Bustos, J.F.
Direct Submission
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Submitted (31-OCT-2000) Research Department, Glaxo Wellcome, S.A
                                                                                                                                                                                                                                                             Dopazo,J., Mendoza,A., Herrero,J., Caldara,F., Humbert,Y., Friedli,L., Guerrier,M., Grand-Schenk,E., Gandin,C., de Francesco,M., Polissi,A., Buell,G., Feger,G., Garcia,E., Pand Garcia-Bustos,J.F.
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Streptococcus pneumoniae
Streptococcus pneumoniae
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Best Local Similarity 65.6%;
Matches 1616; Conservative
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
                                                                                                                                                                                                                             TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357
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                                               GATTGTCAGAGAACCACAATCT---
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                                                                                                                                                                                      GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC
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/mol type="genomic DNA"
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/db_xref="taxon:1313"
/clone="G54"
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                 ATATATGGTTGAGCATACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGA
                                                                                                                        GAAAGGTTTGACCCCTCCTTCGACAGACCATCAGGATTCAGGAAATACTGAGGCAAAAGG
                                                                                                                                                                                                    GATIGGAAAAGATAGCCTTTCIGATAAGGAAAAAGTIGCAGCCTCAAGCCTATACTAAAGA 1725
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                                                                            TGCAGCAGCTATTTACAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCC
                                                                                                                                          AAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAG
                                                                                                                                                                                 GATTAAAAAAGATAGTTTGTCTGAAGCTGAAAGAGCGGCAGCCCAGGCTTATGCTAAAGA
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                                                              AGCAGAAGCTATCTACAACCGCGTGAAAGCAGCTAAGAAGGTGCCACTTGATCGCATGCC
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QY 58 CTATATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG 117	QY 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTTC 57	Query Match 41.3%; Score 987.6; DB 6; Length 2290; Best Local Similarity 67.7%; Pred. No. 1.5e-200; Matches 1481; Conservative 0; Mismatches 645; Indels 60; Gaps 5;	source 1.2290 /organism="unknown" BASE COUNT 766 a 474 c 498 g 547 t 5 others ORIGIN	Fannon, M.R. and Rosen, C.A. Streptococcus pneumoniae antigens and vaccines Patent: US 6159469-A 65 12-DEC-2000; Location/Qualifiers	ified. es 1 to 2290) H., Kunsch,C.A.	ARI20270 ARI20270.1 GI:14103846 Unknown.	RESULT 21 AR120270 AR120270 AR20270 AR	202767 TAA 202		202647 TATGGATAACAATAGTATCATGGCAGAAGCAGAAAATACTTGCCGTTGTTAAAAAGAAG	202587 AAAGGTTGAAGAAAACTGAAGAGAGCTGAAGATTTACTGGAAAAATCCAGGATCCAAT 2036 TCTGAAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAATTTGACTCTTCAAAT		202467 TGAGGAAGAACCCCTCGAGAAGAAAACCGCAAAGCGAGAAACCAGAGTCTCCAAAACC 2126CCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGA	202407 TCAAGCTGATACCAATCAAACGGAAAAAACCAAACGAGGAAAACCTCAGACAGA	202347 TCCGCATTCAGATAATGATTTTGGTAACGCTAGCGATGATGAGAAAAAAAA	202287 GTATACTCTTGAGGATCTTTTGGCGACTGTCAAGTACTATGTCGAACATCCAAACGAACG	202	100
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1126 GGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTC 1185 	AGGCCGCAACCTGCACCAAATCTTAAATTAGATTCTTC	**TTGGGTACCAGATTCAAGGCCAGAACCAAGTCCACAACCCGCAACCTAGTCC	8 AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 	898 AACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCA 957	838 GAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCG 897	778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 837	718 TTCTGTAAGCAATCCAGGAACTACAAATACTAACAAGCAAG	658 AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717	598 GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 657	538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597	478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537 	418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTTGGCACGTTC 477	358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC	298 TGAGGTCAAGGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357 	238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGGATATTGTTAA 297	178 CACTTCACATGGCGACCACTATCATTACAAIGGTAAGGTTCCTTATGACGCTATCAT 237	118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177	64 TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAACTTGACACCAGATGAAGTCAG 123

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                                                                                                                                                                        TCCGCATTCAGATAATGGTTTTGGTAACGCTAGCGACCATGTTCAAAGAAACAAAAATGG
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 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACCATTACCATTCCTAAGAATGA
                                                      GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA
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                                          CCAAGGACGTTATACAACGGATGATGGGTATATCTTCAATGCATCTGATATCATTGAGGA
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PR 31-CCT-1996 US 60/029960

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PC G01N33/68

CC Strandedness: Double;

CC Topology: Linear.
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TGATATAACCAGTGATGAGGGGGGATGCCTATGTAACTCCACATATGACCCATAGCCACTG: 1638
                                                                                       TCAAGTAGCCAAGTTGGCAGGCAAGTACACAACAGAAGACGGTTATATCTTTGATCCTCG
                                                                                                               TCGTATTGCTCAATTAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACA
                                                                                                                                                                                                                                                                                                                                                                TGATAATAAAGGTCGACAAGTTGATTTTGAGGCTTTGGATAACCTGTTGGAACGACTCAA
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REFERENCE
AUTHORS
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Streptococcus antigens
Patent: WO 019834-A 5 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
                                              TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA---TAATCGTGTTTC
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1126 GGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTC 1185 -	958 AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 1017		ADATTCAAGAACCAACTA TOCAGAATACACACACACCACTACAACAACCACACCACTACAACCACACCAC	44 CCAAGGACGTTATACAACGGATGATGGGTATATCTTCAATGCATCTGATATCATTGAGGA 70 38 TACTGGTGATGCTTATATCGTTCCTCATGGAGGATCATTACCATTACATTCCTAAGAATGA 59 1	58 TGCTGCCCACGCGATAACGTCCGTACAAAAGAGGAAATCAATC	118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATGAAGATAACAGACCAAGGCTATGT 177
RESULT 24 AE008464 AE008464 12372 bp DNA linear BCT 13-SEP-2001 LOCUS AE008464 DEFINITION Streptococcus pneumoniae,R6 section 80 of 184 of the complete	168 TCCGCATTCAGATAATGGTTTTGGTAACGCTAGTGACCATGTTCGTAAAAATAAGGCAGA 086 CAGTGAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGAGCAGGAAAAAAAA	1988 TTACAL 1906 TCATTI 2048 CCATTI 1966 CTATTAC 2108 GTATTAC	QY 1726 AAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAG 1785	Db 1688 TCAAGTAGCCAAGTTGGCAGGCAAGTACACAACAGAAGACGGTTATATCTTTGATCCTCG 1747 Qy 1606 TGATATAATCAGTGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTG 1665	1426 TGATGAATCGACTAATAAGAAAAATTGGTAGATGATTATTGGCATTCCTAGCACCAAT	Qy 1186 TCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTCTTGAAAAGCAAGTT 1245

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (27-JUL-2001) Infectious Diseases Research, Eli Lilly and Company, Lilly Research Labs, Indianapolis, IN 46285-0438, USA Location/Qualifiers
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J. Bacteriol. 183 (19), 5709-5717 (2001)
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Streptococcus pneumoniae R6
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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IYGASTGIMAGASLMFFGFLGESISMAVDEVKTPQKNIPRGIVLSLSITVILYALVT
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SLARDGIVPAAFKELTKTISKVPKNATILTGLASAVAAGMFPLASIAAFINICTILAYLI
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KKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRM
PYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGYSLEDLLATVKYYVEHP
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RIIPLRYRSNHWVPDSRPEQPSPQSTPEPSPSPQPAPNPQPAPSNPIDEKLVKEAVRK
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GNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTIELRLPSGEVI
                                        VEVY I LEKENOTDKPS I 1-POFKRNKADENSKLDEKVEBEPKTESKVEKEKLSETGNSTS
NSTLEEVPTVDPVOEKVAKFAES YGMKLENVLFUMDGTI ELY LPSGEV I KKUMADFTG
EAPOGNGENKPSENGKVSTGTVENOPTENKPADSLPBAPNEKPVKPENSTÜNGMLNPE
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5454. .8573
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LDPNLKKSKVKVLBASEGMTLERVPGLEDVEAGDEVDEKTLYDPHTWLDPEKAGEBAO
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KRFGLNOLGIAGISPEQEPSPRQLTEIQEFVKTYKVKTIFTESNASSKVAETLVKSTG
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ESDEKENHVGLNPSADNLYKPSTDT EET EE EAEDTT DEAE IPQVEHSVINAKIAEAEA
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/transī_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label=spr0908
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2683. .5244
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transl_table=11
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/gene="spr0909" 9403. .9543

.9543

gene="spr0909"

'transī_table=11 /label=spr0909 /product="Hypothetical protein"

codon_start=1/ transl_table=

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Matches 1461;
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Best Local
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                     GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTTCCTTATGATGCCATCAT
                                                 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237
                                                                                                                                                                    TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAATTTGACACCAGATGAAGTCAG
                                                                                                                                                                                                        CTATATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG 117
                                                                                                                             CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177
                                                                                                                                                                                                                                                                   TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA---TAATCGTGTTTC 57
                                                                                                                                                                                                                                               Conservative
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NATAESNIETASDENKPSNTRDSKPAESTSENKTTESSTTTGNQEKPVE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (11045. .12265)
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precursor, truncation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-JAN-2001) Department of Bacteriology, Vaccines, 211 Bailey Road, West Henrietta, NY 14586,
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/note="N-terminal truncated
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VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION REFERENCE ACCESSION JOURNAL MEDLINE TITLE AUTHORS SPNEU1907 Streptococcus AL449929 AL449929.1 GI Annotated draft genomic sequence from a Streptococcus pneumoniae type 19F clinical isolate Microb. Drug Resist. 7 (2), 99-125 (2001) 21335329 HTG; HTGS_PHASE2.
Streptococcus pneumoniae
Streptococcus pneumoniae
Bacteria; Firmicutes; Lactobacillales; Dopazo,J., Mendoza,A., Herrero,J., Caldara,F., Humbert,Y., Friedli,L., Guerrier,M., Grand-Schenk,E., Gandin,C., de Francesco,M., Polissi,A., Buell,G., Feger,G., Garcia,E., Prancesco,M., Polissi,A., Buell,G., Prancesco,M., Buell,G., Prancesco,M., Buell,G., Prancesco,M., Buell,G., Buell, and Garcia-Bustos, J.F GI:11545154 75874 bp pneumoniae clone G54, DNA Streptococcaceae, linear SEQUENCING HTG 11-JUL-2001 IN PROGRESS ***. Peitsch, M.

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* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is
* the accession number will be preserved.
Location/Qualifiers
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Direct Submission
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/mol_type="genomic DNA"
/serotype="19F"
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Submitted (31-OCT-2000) Research Department,
Severo Ochoa 2, 28760 Tres Cantos, SPAIN
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is a
* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 702)
Dopazo, J., Mendoza, A., Herrero, J., Caldara, F., Polissi, A.,
Humbert, Y., Friedli, L., Guerrier, M., Grand-Schenk, E., Gandin, C.,
Francesco, M., Buell, G., Feger, G., Garcia, E., Peitsch, M. and
Garcia-Bustos, J.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Annotated draft genomic sequence from a Streptococcus type 19F clinical isolate Microb. Drug Resist. 7 (2), 99-125 (2001)
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                                                                             AAGATGAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAAT 338
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/mol_type="genomic DNA"
/serotype="19F"
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2; Mismatches 17;
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Kunsch, C.A., Choi, G.H., Dillon, P.S., Rose
Fannon, M.R. and Dougherty, B.A.
Streptococcus pneumoniae polynucleotides
Patent: US 6420135-A 243 16-JUL-2002;
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PC C12N5.
PC C12N5.
G06F15/40
CC Stran
CC Topol
FH Key
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JP 2001501833-A/243.
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 TAAGAGGGAGGGGATCAACGCCGAACAAATTGTTATCAAGATTACGGATCAAGGTTATGT
               CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCCAAGGCTATGT
                                                             CTATATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG
                                                                                                             TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA----TAATCGTGTTTC
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                                              TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAACTTGACACCAGATGAAGTCAG
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                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                              Topology: Linear;
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C12N15/09, A01K67/027, C07K14/315, C07K16/12, C12N1/15, C12N1/19,
                                                                                                                                                                                                       a
                                                                                                                                                                                                    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
451 c 511 g 61
                                                                                                                                                                                                                                                               /organism='Unidentified'
                                                                                                                                                      27.4%;
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                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                           Score 653.8; DB 6;
Pred. No. 3.3e-129;
0; Mismatches 413;
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AGCCAAGGATCTTTCAGCAGAAACAGCAGCAGGCATTGATAGCAAACTGGCCAAGCAGGA
                                 TGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGA 1257
                                                                                                                                       AAGTCCGCAACCAGCTCCAAGCAATCCAATTGATGAGAA----ATTGGTCAAAGAAGC
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Sequence
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Choi,G.H., Kunsch,C.A., Barash,S.C., Dillon,P., Fannon,M.R. and Rosen,C.A.
Streptococcus pneumoniae antigens and vaccines Patent: US 6159469-A 181 12-DEC-2000;
Location/Qualifiers
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TAATGTTGCTGTAGCAAGGTCTCAGGGACGATATACGACAAATGATGGTTATGTCTTTAA
                  TGCTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTTTAA
                                                               CAATCGTCAAAAACAAGAACATGTCAAAGATAATGAGAAGGTTA
                                                                                    CAATCGACAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGG
                                                                                                                                                                                                                                                                                   GGTTCCTTATGACGCTATCATCAGTGAAAGAATTACTCATGAAAGATCCAAACTATAAGCT
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CC Topology:
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Kunsch,C.A., Choi.G.H., Johnson,S.L. and Hromockyj,A.

Streptococcus pneumoniae antigens and vaccines

Patent: JP 2001505415-A 91 24-APR-2001;

HUMAN GENOME SCIENCES INC

PN JP 2001505415-A/91
                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae
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BD063337.1 GI:22608940
JP 2001505415-A/91.
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I CHARLES A KUNSCH,GIL H CHOI,SYDNOR L JOHNSON,ALEX HROMOCKYJ

C12N15/31,C12N5/18,C12N1/21,C07K14/315,C12Q1/68,A61K39/09, PC
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Streptococcus pneumoniae proteins and nucleic Patent: WO 02077021-A 1987 03-OCT-2002;
Chiron Spa (IT): THE INSTITUTE FOR GENOMIC RE Location/Qualifiers
1. .3117
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TTCAAGAACAAACTGGGTACCTTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAG
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/mol type="genomic DNA"
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_526 c 612 g 829 t
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Submitted (03-NOV-2000) Molec
West Watkins Mill Road, Gaith
Location/Qualifiers
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Adamou, J.E., Heinrichs, J.H., Erwin, A.L., Walsh, W., Gay
Adamou, J.E., Heinrichs, J.H., Erwin, A.L., Walsh, W., Gay
Dormitzer, M., Dagan, R., Brewah, Y.A., Barren, P., Lathig
Langermann, S., Koenig, S. and Johnson, S.
Identification and characterization of a novel family
pneumococcal proteins that are protective against seps
Infect. Immun. 69 (2), 949-958 (2001)
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Streptococcus pneumoniae
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/protein_id="AAK06761.1"
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/db_xref="G1:12744746"
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SCLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYYVLKDAAHADNVRTKDEINRQKQEH
VKDNEKVNSNVAVARSQGRYTTNDGYVFNPADIIEDTGNAYIVPHGGHYYIPKSDLS
ASELAAAKAHLAGKNNQPSQLSYSTASDNNTQSVAKGSTSKPANKSENLQSLLKELY
DSPSAQRYSESDGLVFDPAKIISRTPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPI
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/mol_type="genomic DNA"
/serotype="4"
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/transl_table=11
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USA
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                    ATACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGGAAAT
                                                                                       AAAAGATGAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAA
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 ATATTATGTCTACCTGAAAGATGCAGCTCATGCTGATAATGTTCGAACTAAAGATGAAAT
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IVHHGDHFH/IPKSNOJGQPTLPNNSLATPSPSLFINPGTSHEKHEEDGYGFDANRII
AEDESGFVMSHGDHNHYFFKKDLTEEQIKAAQKHLEEVKTSHNGLDSLSSHQQDYPSN
AKEMKDLDKKLEEKIAGIMKQYGVKRESIVVNKEKNAIIYPHGDHHADPIDEHKPVG
IGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNVVNLLKNSTFNNQNFTLANGQKRVS
FSFPFELEKKLGINMLVKLITDGKKVLEKVSGKVFGEGVANAFLDDAPYLFQGTFK
YTIASKDYPBVSYGTGTTVPTSLAYKMASQTIFYFHAGDTYLRVNPQFAPYRTDAL
VRVFDEFHGNAYLENNYKVGEIKLPFKLNQGTTRTAGNKIPVTFMANAYLDNQSTYI
VEVPILEKENQTDKPSJLAPGKNKAQENIKLDBKVEEPKTSEKVEEKILSETGNSTS
NSTLEEVFTVDPVQEKVAKFAESYGMKLENVLFNDGTIELYLPSGEVIKNMADFTG
EAPQCNGENKSSENGKVSTGTVENQFTENKADSLPEAPNEKPKYEKKLESTGNSTS
NSTLEEVFTVDPVQEKVAKFAESYGMKLENVLFNDGTIELYLPSGEVIKNMADFTG
EAPQCNGENKSSENGKVSTGTVENQFTENKADSLPEAPNEKPVKEEKILSETGNSTS
NGTLEEVFTVDPVQEKVAKFAESYGMKLENVLFNDGTIELYLPSGEVIKNMADFTG
EAPQCNGENKSSENGKVSTGTVENQFTENKADSLPEAPNEKPVKEENTSNAMAVENDFTG
EAPQCNGENKSSENGKVSTGTVENOFTENKADSLPEAPNEKPVKEENTSNAMADFTG
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/note="Region:
925. .942
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/note="Region: histidine
522. .789
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/note="Region:
1648. .1665
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1569. .1749
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/note="Region: histidine
1414. .1491
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247. .264
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/gene="phtE"
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1381. .1398
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Indels

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REFERENCE
AUTHORS
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AX343070
LOCUS
DEFINITION
ACCESSION
                                                            BASE COUNT
ORIGIN
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ORGANISM
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                                                                                                                                                                      FEATURES
Query Match 16.1%;
Best Local Similarity 65.3%;
Matches 631; Conservative
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Sequence 1
AX343070
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                                                                                                                                                                                                                                                                            unidentified unidentified
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                                                                                       /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
/note="BVH-3"
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from Patent WO0198334.
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Score 385.4; DI
Pred. No. 7.6e-
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SHIRE BIOCHEM INC. (CA)
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                                                                                            ATCTGGTCGAGGAAATCTGTCAAATTCAAGAACCTATCGCCGACAAAATAGCGGATAACAC
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Kunsch (C.A., Choi,G.H., Dillon,P.S., Rosen,C.
Fannon,M.R. and Dougherty,B.A.
Streptcocccus pneumoniae polynucleotides and
Patent: US 6420135-A 192 16-JUL-2002;
Location/Qualifiers
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Topology:
Key
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                                                                        C12N1/21
                                                                                    MICHAEL FANNON, BRIAN A DOUGHERTY
C12N15/09, A01K67/027, C07K14/315, C07K16/12, C12N1/15, C12N1/19,
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30-OCT 1997 JP 1998520718
31-OCT-1996 US 60/029960
CHARLES A KUNSCH,GIL H CHOI, PATRICK J DILLON, CRAIG
                                                                                                                                                                                    Unidentified JP 2001501833-A/192
                            Strandedness: Double,
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                    TCCAGCACAAATCACAAGTCGAACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTA
                                                        GGĂACTCTATGATTCACCTAGCGCCCĂACGTTACAGTGAATCAGATGGCCTGGTCTTTGA
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
1325 c 1212 g 243
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Pred. No. 7.4e-72;
0; Mismatches '276;
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AR219123
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Kunsch,C.A., Choi,G.H., Dillon,P.S., Rose
Fannon,M.R. and Dougherty,B.A.
Streptococcus pneumoniae polynucleotides
Patent: US 6420135-A 355 16-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unclassified
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TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACCATTACCATTCCTAAGAATGA
                                           CCAAGGACGTTATACAACGGATGATGGGTATATCTTCAATGCATCTGATATCATTGAGGA
                                                          GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA
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                                                                                                                  TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTC
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Pred. No. 5.6e-71;
0; Mismatches 131;
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Fannon,M. and Dougherty,B.A.
Polynucleotide of Streptococcus pneumoniae and
Patent: JP 2001501833-A 355 13-FEB-2001;
HMAN GENOME SCIENCES INC
Unidentified
PN JP 2001501833-A/355
PD 13-FEB-2001
PF 30-OCT-1997 JP 198520718
PR 31-OCT-1996 US 60/029960
PI CHARLES A KUNSCH,GIL H CHOI,PATRICK J DII
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R 31-OCT-1996 US 60/029960
I CHARLES A KUNSCH,GIL H CHOI,PATRICK J DILLON,CRAIG
STEVEN C BARASH,
                                                                                                CACTTCACATGGCGACCACTATCATTACTATTACGATAGGTTAAGGGTTCCTTATGACGCTATCAT
TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA
                                                    CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA
                                                                               GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTTCCTTATGATGCCATCAT
                                                                                                                                      TAAGAGGGAGGGGATCAACGCCGAACAAATTGTTATCAAGATTACGGATCAAGGTTATGT
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C12N15/09, A01K67/027, C07K14/315, C07K16/12, C12N1/15, C12N1/19,
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
178 c 211 g 25
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Pred. No. 5.6e-71;
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Patent: WO 0198334-A 9
SHIRE BIOCHEM INC. (CA)
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                                                                                                                                                                                                                                                                        Tettelin,H., Nelson,K.E., Paulsen,I.T., Eisen,J.A., Read,T.D., Peterson,S., Heidelberg,J., DeBoy,R.T., Haft,D.H., Dodson,R.J., Durkin,A.S., Gwinn,M.C. Kolonay,J.F., Nelson,W.C., Peterson,J.D., Umayam,L.A., White,O., Lewis,M.R., Radune,D., Holtzapple,E., Khouri,H., Wolf,A.M., Utterback,T.R., Hansen,C.L., McDonald,L.A., Feldblyum,T.V., Angiuoli,S., Gesuwan,P., Hickey,E.K., Holt,I.E., Loftus,B.J., Ujwal,M.L., Yang,F., Smith,H.O., Venter,J.C., Dougherty,B.A., Morrison,D.A., Hollingshead,S.K. and Fraser,C.M.
                                                                                                                                                                                        Submitted (29-JUN-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
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Science 293 (5529), 498-506
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/gene="SP1005"
/note="This region contains a gene with one or more
premature stops or frameshifts, and is not the result of
                                                               /db_xref="taxon:170187"
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NATAESNIETASDENKPSNTRDSKPAESTSENETTESSTTTGNQEKPVE"
                                                                                                                                                                                                                              NTDSRLIDALVNTVRVNENQEFKEFLPEEETFDELVPSDETKNILAESQDLQMPEFVK
KLIEKKGRENVKMPYLIKKMLEKAGKLPKE"
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1612. .2241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPDKTMFVQDAIRFAQQHGFNML"
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                                                                                                                                                       complement (4791.
                                                                                                                                                                                                      complement (4791.
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TIGR00109"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="
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protein_id="AAK75122.1"
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     conductance mechanosensitive channel
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                                                                                                                                                                         I (bases 1 to 1684)
Kunsch, C.A., Choi, G.H., Dillon, P.S., Rose
Fannon, M.R. and Dougherty, B.A.
Streptcocccus pneumoniae polynucleotides
Patent: US 6420135-A 258 16-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                            Sequence
AR219026
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/note="This region contains an authentic frame shift and is not the result of a sequencing artifact; similar to GP:2804700; identified by sequence similarity; putative; IS1167, transposase, authentic frameshift"
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OS Unidentified
PN JP 2001501833.A/25
PD 13-FEB-2001
PF 30-OCT-1997 JP 199
PR 31-OCT-1996 US
PI CHARLES A KUNSCH,G
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PC C12N1
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I MICHAEL FARNON, BRIAN A DOUGHERTY

C C12N15/09,A01K67/027,C07K14/315,C07K16/12,C12N1/15,C12N1/19,

C C12N1/21,

C C12N5/10,C12P21/02,C12Q1/68,G06F17/30,C12N15/00,C12N5/00, PC
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31-OCT-1996 US 60/029960
CHARLES A KUNSCH,GIL H CHOI, PATRICK
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Qy 420 GTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCT	QY 360 CTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC	QY 300 AGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATG 359	OY 240 GTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATG 299	QY 180 CTTCACATGGCGACCACTATCATTACTACGATAGGTACGCTTATGACGCTATCATCA 239	QY 120 AGCGTGAAGGAATCAATGCTGAGCAAATCGTCAAGATAACAGACCAAGGCTATGTCA 179	QY 60 ATATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCA 119	Query Match 9.2%; Score 219.6; DB 6; Length 75248; Best Local Similarity 48.0%; Pred. No. 1.9e-36; Matches 1083; Conservative 0; Mismatches 1045; Indels 127; Gaps 11;		SCIENTIFIQUE (CNRS) (FR) FEATURES . Location/Qualifiers source 175248 //Organism="Streptococcus agalactiae"	TITLE Streptococcus agalactiae genome sequence, use for developing vaccines, diagnostic tools, and for identifying therapeutic targets JOURNAL Patent: WO 02092818-A 13 21-NOV-2002; INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE	REFERENCE 1 AUTHORS Glaser, P., Rusniok, C., Chevalier, F., Frangeul, L., Lalioui, L., Zouine, M., Couve, E., Buchrieser, C., Poyart, C., Trieu-Cuot, P. and Kunst, F.	SOURCE Streptococcus agalactiae ORGANISM Streptococcus agalactiae Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.	ITION Sequence 133 from Patent WO02092818. SION AX602204 ON AX602204.1 GI:28402073 RDS	7	Qy 2322 AAGCAGAAAATTACTTGCGTTGTTAAAAGGAAGTAA 2358	OY 2262 TAGCTGGTTTACGAAATATTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAG 2321	Qy 2202 CAGAAGTTTTGCTTGCGAAAGTAACGGATTCTAGTCTGAAAGGCCAATGCAACAGAAACTC 2261
Db 21394 AAACAGCTCAAGAAATCTATGAGCAATTGAACCAAAAGCAATTGTTAAACCTGAAGATT 21335	1347 AGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACA	OY 1287 AAGAAAAIGTTGCTCCTCGTGACCAAGAATTTTATGATAAAAAGCATATAAATCTGTTAACTG 1346	227 AMARIC I ISANANG CARGA I A CAMPACAMANG I SI I I CACACAC I I I ACCIDENTAMA	. 22	, 21 1	Db 21744 CAGAGAAACCAAAGCATATTCTCATGAACCTAATAAGGAACCTCACACAGAGGAAGCAAATCTTAAAA 1106	21	927 GAGATCATTACCACTTCATCCCCTTACTCTCAAATGTCTGAATTGGAAGAACGAATCGCTC	Qy 867 TIGICITITGATCCAGCACAAATCACAAGTCGAACAGCTAGAGGTGTTGCAGTGCCACACG 926	Oy 807 GTCTCTTGAAACAGCTCTACAAACTGCCTTTGAGTCAACGACATGTAGAATCTGATGGCC 866	Qy 747 CTAACACAÁGCAACAACAGCAACACTAACAGTCAAGCTAAGTAATGACATTGATA 806	Qy 722	OY 672 ATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTCT721	Qy 631	OY 573 ATTACCATTACATTCCTAAGAATGAGTTATCAGCTAGGGAGTTGGCTGCAGAAGC 630	Oy 513 TTAATGCTTCTGATATCATAGAGGATACTGGTGATGATGATCTTATATCGTTCCTCATGGAGATC 572	Qy 461GTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCT 512

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                                                       Glaser P., Rusniok, C., Chevalier, Zouine, M., Couve, E., Laliui, L., Trieu-Cuot, P. and Kunst, F. Genome sequence of Streptococcus invasive neonatal disease
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                                                                                                                                    Glaser, P.,
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Glaser, P., Rusniok, C. and Frangeul, L.
Direct Submission
Submitted (31-MAY-2002) Glaser P., Institut Pasteur, General Microorganismes Pathogenes, 25, rue du Docteur Roux, 757 Cedex 15, FRANCE. E-mail: pglaser@pasteur.fr Phone: +33 89 96, Fax: +33 (0)1 45 68 87 86
Location/Qualifiers
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ARNYVRRVGELVGVRISTFSVGPGREQTNILESVWSNI"
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7504.
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IRIAPELKPFYHNIQDDHFAILKKIEEADNKAELAAIHQANMKRFTDVLAGYIRIKQS
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6700. .7518
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7515. .8771
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the N_terminal part) and to cyanophycinsynthetase
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1309. .6608
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1324. .6576
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1309. .4314
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                                                                                                           product="Unknown"
                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                note="Similar to other proteins"
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                                                                                                                                GTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCT-----
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                                                                                   CTAAGGGTGGTTCTAAGGGAGAATCAGGAAAAGCATAGTAGTGCAAAAACTCAAGCTTTAT
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LLKNANRELNGFIAKYKDATPAELEKKPNLIQKLFKQSKTSLQEFYFDSQNIEQKMDM
MAANVVKQEDTLARNIVSAEMLIEDNTKSIENLVGVIAFIESSQAEAANRASHLQQEI
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9770. .10747
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LLDDEDKVKVAGGFMLQVLPGASDEEISRYEKRIQEMPSISSLLESENHIESLLSAIY
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RQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTADAIVNANNAALQMLAETSKEAIP
MLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGRKERAQLESAVIKSAETINDS
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TLIANQILAANQKGNSKVTVKVIGDSSFGHIISVADTKGNVKGYIQNTGVDIKKTATG
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                                       - GTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCT
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/note="Similar to transcription regulator"
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/transl_table=
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/note="Similar to other proteins"
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/db_xref="GI:24413446"
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CTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATTAGCTGATAAGTATACAA 1577
                                      TATTATTTGGAATTGCACAAGCGACAGACTATAAGAATGGTACATTTGTAATTCCTCATA
                                                                             ATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG---ACTTGGCAAACCAAATT
                                                                                                                                                 AATTATTAGAACGCTTGAATGA------TGAATCGACTAATAAAGAAAAATTGGTAGATG
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                                                                                                                                                                                                                                                                                                                                                  AAGAACCTGAAGATTCAGGGAAAGTAACTCACAACTATGGTTTTTATGATGTTAATAAAG
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Query Match
                                                                                                                                                                Koenig,S., Heinrichs,J., Johnson,L.S. and Adamou,J.E. Homologs of a pneumococcal protein and fragments for vaccines Patent: WO 0114421-A 1 01-MAR-2001;
                                                                                                                                                                                                                                                   Streptococcus pyogenes
Streptococcus pyogenes
Bacteria; Firmicutes; Lactobacillales;
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                                                                                                                                                                                                                                       Streptococcus.
                                                 846
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/db_xref="taxon:1314"
486 c 518 g 628
                                                                                                                                  Location/Qualifiers
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Score 214.6;
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 2478;
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Local

Similarity

60.8%;

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AUTHORS
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Streptococcus pyogenes
Bacteria; Firmicutes; I
                                                                Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Sezate,S.S., Surcorov,A.N., Kentcon,S., Lai,H., Lin,S., Qian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
Complete genome sequence of an M1 strain of Streptococcus pyogenes
                                                                                                                                                                                                   streptococcus.
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Retrietti,J.J., McShan, W.M., Adjic,D., Savic,D., Savic,G., Lyon,K.,

Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S.,

Qian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J.,

Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-APR-2001) Department of Microbiology University of Oklahoma Health Sciences Center, 940 Oklahoma City, OK 73104, USA Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGNHYMIPKKDLSPSELAAAQAYWSQKQGRGARPSDYRPTPAPAPGRRKAPIPDVTP
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                                                                                                                                                                                                                                                                                                                                                                                                        HYIGFGELBQYELDBVANWKAKGQADELAAALDQEQGKEKPLPDTKKVGRKVTKDGK
VGYMMPKDGKDYFYARDQLDLTQIAFAEQELMLKOKKHYRYDIVDTGIEPRLAVDVSS
LPMHAGNATYDTGSSEVIPHIDHIHVYPYSWLTRDDIATIKYMVQHPBVRDDIVKKPD
HEBSGSVIPNVTPLDKRAGMPNWQIIHSAEEVQKALAEGRFATPDGYIFDPRDVLAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Best Blastp hit = gb|AAB58414.1| (AF000561) interacting peptide 21; TIP21; Transcription Termin Factor I Interacting Peptide 21 [Homo sapiens]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SPy2005"
complement (71.
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complement(71. .271)
                                                                                                                                                                                                                                                          complement (2930.
                                                                                                                                                                                                                                                                              /gene="lmb"
/note="synonym:
                                                                                                                                                                                                                                                                                                                        complement (2930.
                                                                                                                                                                                                                                                                                                                                              QPEGVQFYNKNGELVTYDIKTLQQINP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SPy2006"
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/protein_id="AAK34687.
/db_xref="GI:13623018"
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/transl_table=
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                                                                                                                                                                                                                                  gene="lmb"
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1ypothetical protein SCF91.38c. [Streptomyces coeli
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Young Blvd,
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VPHFTTYGKNYSRRFQEKGLIESIFTHIYGLCHTGLIFBLIGHTHIKANANNRK
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KQLTETATVKTADQDKEMPULSTNREBPNKAYDYAYANGMKEDDFKDVKGKIALIE
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AKQDDDSHYYIHRHANGKPYAALSPNGGONDTVYQFGQGTFLRNACHVABVLDKEGNV
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                                                                        Terao, Y., Kawabata, S. and Hamada, S. Characterization of a novel histidine triad
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Streptococcaçeae;

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BCT 03-NOV-2001

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax:81-6-6878-4755)
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    TAGTCAACATCGTGAAG---
                                          AGGTAGCAAGCGCAAAAACATTCGAACCAAACAACTTGCTGAGCAAGTAGCCAAAGG
                                                                                TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA
                                                                                                                                                                                                    TAGCGAAGAGTTGTTGATGACGGATCCTAATTACCGTTTTAAACAATCAGACGTTATCAA
                                                                                                                                                                                                                                            CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA
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VGYMMPKDGKDYFYARDQLDLTQIAFABQELMILKOKKHYRYDIVDTGIEBRLANDVSS
LPMHAGNATYDTGSSEVIPHIDHIHVVPYSWITRDQIATIKYVMQHPEVRPDITWKFD
HEESGSVIPNVTPLDKRAGMPNWQIIHSAEEVQKALAEGRFATPDGYIFDPRDVLAKE
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GLIFEPTQVIKSNAFGYVVPHGDHHHIIPRSQLSPLEMELADRYLAGQTEDDDSGSDH
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SEELLMTDPNYRFKOSDVINEILDGYVIKNGKNYVYYLKPGSKKRNIRTKOQIAEQVA
KGTKEAKEKGLAQVAHLSKEEVAAVNEAKRQGRYTTDDGYIFSTDIIDDGDAYLVD
HGNHYHYIPKKDLSPSELAAAQAYWSQKQGRGARPSDYRPTPAPAPGRRKAPIPDVTP
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/mol type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="histidine triad protein of group A streptococci"
/protein id="BAB71774.1"
/protein id="BAB71774.1"
/db_xref="GI:16610230"
/translation="MKKTYGYIGSVAAILLATHIGSYQLGKHHMGSATKDNQIAYIDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=
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/strain="SSI-9"
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Smoot, J.C., Barbian, K.D., Van Gompel, J.J., Smoot, L.M.,
Smoot, J.C., Barbian, K.D., Sturdevant, D.E., Ricklefs, S.M.,
Chaussee, M.S., Sylva, G.L., Sturdevant, D.E., Ricklefs, S.M.,
Porcella, S.F., Parkins, L.D., Beres, S.B., Campbell, D.S., Smith, T.M.,
Zhang, Q., Kapur, V., Daly, J.A., Veasy, L.George. and Musser, J.M.
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Smoot, J.C., Barbian, K.D., Van Gompel, J.J., Smoot, L.M.,
Chaussee, M.S., Sylva, G.L., Sturdevant, D.E., Ricklefs, S.M.,
Porcella, S.E., Parkins, L.D., Beres, S.B., Campbell, D.S., Smith, T.M.,
Zhang, O., Kapur, V., Daly, J.A., Veasy, L.G. and Musser, J.M.
Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes MGAS8232
Streptococcus pyogenes MGAS8232
Bacteria; Firmicutes; Lactobacillales;
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Streptococcus
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complement(95..259)
/gene="spyM18_2063"
complement(95..259)
/gene="spyM18_2063"
/note="best blastp match h
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LADYRMKIET"
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/db_xref="GI:19749145"
                gene="SMEZ"
                                                                                                                                                                                                                                                                                                                          /mol_type="genomic
/strain="MGAS8232"
                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                                                                                                              codon_start=1/
transl_table=
note="synonym: spyM18_2064"
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20 В Ś B Ş В Ś Ъ S

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PKTPIKDNKVAKAKQLLTKAGWKEQADGSRKKGDLDAAFDLYYFTNDQLRANLAVENA
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FYNNFTVTKYLDKAMTSSDLDKANEYWKLAQWDGKTGASTLGDLPNVWLVSLNHTYIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="mitogenic exotoxin Z precursor"
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                                                                                           SSEYVLFARARGETQWQIFKHHCLRNAIVPAITLHFSYFGELFGGSVLAEQVFSYPGL
GSTLTEAGLKSDTPLLLAIVMIGTLFVFAGNLIADILNSIINPQLRRKV"
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SFILMGLSWILIGGLIGFILGTTLSAFHQGKLLDRIVRWFSYLOJISVPTFUSDIIRSRAGA
SFILMGLSWILIGGLISSPIGTLSQDITLADRIKHLMLPVFTLSILGIANVTLHTRTKMMSVL
                                                                                                                                                                                                                                                                                                                                                           pyogenes] "
                                                                                                                                                                                                                                                                                                                                                                                    /note="best blastp match gb|AAC67218.1| (U78968)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKRINVGKQGVHSHGHDWSLLTNIAEWTWDESTK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KWTWVLLDENTALAALESGDVDMIYATPELASKKVKGTRLLDIPSNDVRGLSLPYVKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLHDDFKFSNGEPVTADDVKFTYDMLKADGKAWDLTFIKNVEVVGKNQVNIHLTBAHS
TFTAQLTEIPIVFKKHYNDKYKSNPIGSGPYMVKEYKAGEQAIFVRNPYWHGKKPYFK
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VSMGAKLPHEFDPKDRYGVHNEGNITHSTLLKRSPELDIKGELAKTYHLSEDGLTWSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (1334...1468)
/gene="spyM18_2065"
complement (1334...1468)
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FNIDKIGHLDIEIDS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3388.
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/note="best h7--
                                           'gene="dppC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="dppB"
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/transl_table=
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1362. .5183
                                                                                                                                                                                                                                           db_xref="GI:19749149"
                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="dpp8"
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table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MTYFRLKKELNWSLRNKGIVVYEGNQKLQIAINTGKNNSEKSLF
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               spyM18_2068"
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Z [Streptococcus pyogenes M1 GA
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/note="best blastp match gb|AAK34684.1| (AE006622)
transmembrane transport protein [Streptococcus pyogenes M1
GAS]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tränslation="WTLBAKKIGFYHKKDOWLFKEIDLEVAGGOLIGIFGQSGCGKTS
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hypothetical protein (Streptococcus pyogenes M1 GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="best blastp match gb|AAK34686.1| (AE006622) ATPase
protein [Streptococcus pyogenes M1 GAS]"
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ISDTVSLIIADEPTPGLHPDALQMVLDQLRSFADKGISVIFITHDIVAASQIADRITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein (Streptococcus pyogenes M1 GAS)
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APSLAHLFGTDGLGRDMFVRTIKGLYFSLGVGLLGALMGVFLLATVFGVLAGLGNSLID
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ypothetical protein [Streptococcus pyogenes M1 GAS]"
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                                                                                                                                                                                                                                                                      gene="spyM18_
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product="hypothetical
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/note="synonym:
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REFERENCE
AUTHORS
TITLE
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ORGANISM
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VERSION
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                                                        SAG290952

Ostreptococcus agalactiae lmb gene for protein, partial ORFy and partial in AJ290952

AJ290952

AJ290952.1 GI:13548638

adhesin; insertion sequence IS1548; protein; lmb gene; orfy.

Streptococcus agalactiae

Streptococcus agalactiae
Bacteria; Firmicutes; Lactobacillale
                                                                                                                                                                                                                                                                                                                                                                                                                                       514
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 Granlund,M., Michel,F. and Norgren,M. Mutually exclusive distribution of IS1548 and
                                                Streptococcus.
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                                                                                                                                                                                                                                                                                                                                          TAGTCAACATCGTGAAG-------GTGGAACTCCAAGAAACGA
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                                                                                                                                                                                                                                                                                                                                                                       TTACCATTACATTCCTAAGAATGAGTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                       TAGTCCGACAGATATCATTGATGATTTAGGAGACGCTTATTTAGTACCTCATGGTAATCA
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HGNHYHYIPKKDLSPSELAAAQAYWSQKQGRGARPSDYRPTPAPGRRKAPIPDVTPNP
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                                                            Lactobacillales;
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Pred. No. 5.1e-35;
D; Mismatches 230;
                                                                                                                      IS1548; laminin-binding
                                                                                                                                                                DNA linear BCT 07-JUI for laminin-binding surface insertion sequence IS1548.
                                                            Streptococcaceae
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TITLE
                                                                                                                             Query Match
Best Local Similarity
                                                                                                             Matches
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 64
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Direct Submission
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J. Bacteriol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                group II intron identified in human isolates
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AGATGGAAAACAAGCGACGCAAAAA-----ACGGAGAATTTGACTCCTGATGAGGTTAG 117
                                    TTACCAGCTTGGTAAGCATCATATGGGTCTAGCAACAAAGGACAATCAGATTGCCTATAT
                                                                       TTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTATAT
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KQLGISGISPEQEPSPRQLKEIQDFVKEYNVKTIFAEDNVNPKIAHAIAKSTGAKVKT
                                                                                                                                                                                                      GQGHQPDNGGYHP"
366 c 4
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40. .45
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/mol_type="genomic DNA"
/isolate="5531"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSPLEAAPSGNKTYLENLRANLEVLYQQLK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="serotype III"
insertion_seq="IS1548"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            country="Sweden:Umea"
note="serotype III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="ORFy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function="putative
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60.5%;
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                                                                                                         0;
                                                                                                         Score 211.4; DB 1
Pred. No. 1.2e-34;
0; Mismatches 231
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Umea
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                                                                                                           Indels
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Db 1769 C 1769 Search completed: November 13, 2003, 23:47:14 Job time : 8825 secs	Qy 634 C 634	Db 1709 CTATCATTATATTCCTAAAAAGGATTTGTCTCCAAGTGAGCTAGCT	QY 574 TTACCATTACATTCCTAAGAATGAGTTATCAGCTAGCGAGTTGGCTGCAGAAGCCTT	Db 1649 TAGTCCGACAGATATCATTGATGATTTAGGAGATGCTTATTTAGTACCTCATGGTAATCA	OY 514 TAATGCTTCTGATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCA	Db 1589 TGCGGCAGTCAATGAAGCAAAAAAGACAAGGACGCTATACTACAGACGATGGCTATATTTT	QY 454 TGGTGCTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTT	Db 1529 AACTAAAGAAGCTAAAGAAAAAGGTTTAGCTCAAGTGGCCCATCTCAGTAAAGAAGAAGA	QY 418 TAGTCAACATCGTGAAG	Db 1469 AGGTAGTAAGCGCAAAAACATTCGAAACCAACAAATTGCTGAGCAAGTAGCCAAAGG	QY 358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAAATCAATC	Db 1409 TGAAATCTTAGACGGTTATTAATAGTCAATGGCAACTATTATGTTTACCTCAAGCC	Qy 298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA	Db 1349 TAGTGAAGAGTTGTTGATGACGGATCCTAATTACCGTTTTAAACAATCAGACGTTATCAA	Qy 238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA	Db 1289 GACCTCACACGGTGACCATTATCATTTTTACAATGGGAAAGTTCCTTATGATGCGATTAT	QY 178 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT	Db 1229 TGCTGAAGAAGGCATCTCTGCTGAACAGATCGTAGTCAAAATTACTGACCAAGGCTATGT	QY 118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT	Db 1169 TGATGATAGCAAAGGTAAGGTAAAAGCCCCCTAAAACAAAC
		AAGTGAGCTAGCTGCACAAGCCTA 1768	TAGCGAGTTGGCTGCAGAAGCCTT 633	TGCTTATTTAGTACCTCATGGTAATCA 1708	TGCTTATATCGTTCCTCATGGAGATCA 573	CTATACTACAGACGATGGCTATATTTT 1648	CTATACTACAGATGATGGTTATATCTT 513	AGTGGCCCATCTCAGTAAAGAAGAAGT 1588	GTGGAACTCCAAGAAACGA 453	ACAAATTGCTGAGCAAGTAGCCAAAGG 1528	GGAAATCAATCGACAAAAACAAGAGCA 417	TGGCAACTATTATGTTTACCTCAAGCC 1468	TGGAAAATACTATGTTTACCTTAAGGA 357	CCGTTTTAAACAATCAGACGTTATCAA 1408	TAAGCTAAAAGATGAGGATATTGTTAA 297	TGGGAAAGTTCCTTATGATGCGATTAT 1348	TGGTAAGGTTCCTTATGACGCTATCAT 237	AGTCAAAATTACTGACCAAGGCTATGT 1288	CATCAAGATAACAGACCAAGGCTATGT 177	AACAAACAAAACGATGGATCAAATCAG 1228

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Result
No.
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Maximum Match 100%
Listing first 100 :
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
2388
2388
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1374.2
                                                                                                                                           Score
                                                                                                                                                                                                                                                                          N Geneseq 19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

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                                                                                                protective or therapeutic
                                                                            Claim 1;
                                                                                                                       Nucleic
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                                                                                                                                                                                                   HUMAN GENOME SCI INC.
                                                                            Page
                                                                                                                                                                            Hromockyj
                                                                                                          encoding antigenic peptide(s) from Streptococcus or their epitope-containing fragments, useful in
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amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.
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Length 2389; 0, Gaps

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The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment,
                                                                                                                                                                      WPI; 2003-040579/03
                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae type 4 strain
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABX06886 standard; DNA; 2406 BP
                                                                                              New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
                                                                                                                                                                                                  Masignani V,
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                                                      Claim 6; SEQ ID No 2347; 56pp; English
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infection; antiinflammatory; antibacterial; immunostimulant;
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Streptcoccus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification
                                 primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted is SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays pharmaceutical compositions and vaccines for Streptococcus
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Sequence 8195 BP; 2688 A; 1622 C; 1777 G; 2105 H 3 other;

DB 19;

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Query Match Best Local Similarity

Ş 밁 Ş 밁 S 멍 Ş 밁 á 뭉 Š 밁 Ş Matches 3173 3293 3233 3113 3053 181 2388; 301 241 121 361 61 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360 TGAAGAATTACTCATGAAAGATCCAAACTATAAAGCTAAAAGATGAGGATATTGTTAATGA 300 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA TATAGATGGAAAAACAAGCGAAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 3352 100.0%; Score 2388; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches <u>بر</u> Indels 0; Gaps 3232 180 3172 3112 3292 60 0

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1321 TGATAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380	4444	4073 GTACCAGATTCAAGGCCAGAACCAAGTCCACAACCGAACCCGAACCCAGTCCAGGCCAAGTCCAGGG 4132 1081 CCCGCAACCTGCACCACATCTTAAAATAGACTCAAATTCTTCTTTTGGTTAGTCAGCTGGT 1140	3953 AGCTAGAGGTGTTGCAGTGCCACGAGATCATTACCACTTATCCTTTACTCTCAAAT 4012 961 GTCTGAATTGGAAGACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020	901 AGCTAGAGGTGTTGAGTGCCACAGGCCACAGAGCTCCAGAAACTGCCTTTGAG 3892 901 TCAACGACATGTAGAATCTGATGGCCTTGTTTGATCCAGACACAAATCACAAGTCGAAC 900 3893 TCAACGACATGTAGAATCTGATGGCCTTGTTTTGATCAGCACAAACTCACAAGTCGAAC 3952 901 AGCTAGAGGTGTTGCAGTGCCACACGAGAGAGATCATTACCACATCCCTTACTCTCAAAT 960	721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAACAACAACAACAACAACAACAACA	601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660	481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540	
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RESULT 6 ABS56454/c ID ABS56454 standard; DNA; 2162598 BP. XX XX AC ABS56454; XX DT 10-FEB-2003 (first entry) XX	Qy 2281 TTTGACTCTCAAATTATGGATAACAATAGTATCATGGCAGAAAGAGCAGAAAATTACTTGC 2340	Oy 2161 TCAAGTAGAGACTGAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGC	2041 TGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAGACCACAGTGCAAGATCCAAA 2	1921 TAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGGAAGA	Qy 1801 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1860	Qy 1681 CCTTTCTGATAAGGAAAAACTTGCACCTCAAGCCTATACCTAAAGAAAAAGGTATCCTACC 1740	156. AGCTR 4613 AGCTR 1621 TGAAG 4673 TGAAG	4493 TAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1501 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT

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                                                                                                                                                                                                                                                                Rational and the machine of the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers thaving substantial complementarity define the termini of the target sequence, and where the parts of the primers having substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis media or ear infection. They are also useful in developing vaccines, diagnostics and antibotics. The methods are useful for identifying immunodominant proteins. The methods are useful for Streptococcus pneumoniae type 4 strain genome sequence is the streptococcus data for this patent did not form part
                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56494. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides and second primers.
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TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC
                                                              AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA
                                                                                                                          TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCCTTGCGAA
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                  Matches 1819;
                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptcoccus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptcoccal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence encodes the s. pneumoniae BVH-11 protein antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal; ds.
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P-PSDB; AAB12716.
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GGAAGAAACCCCTCGAGAAGAAACCACAAAGCGAGAAACCAGAGTCTCCAAAACCAACC	1969 TRACCATRACATURAGATTIGAGIGGETTAGGAGGCCTTIA IGAGGCCCTARAGGGTA 2039 1969 TACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGAAAAAAAA	89 AGCAGCTATTITACAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCCACTA	1609 TATAATCAGTGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGAT 1668	1500 TGTCTCAAGTGATAAAGTCAAGTTAGTGGATGATATTCTTGCTCTTAGCTCCGATTCG 1559 1489 CCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATTGAGTATACCTGAAGACGAAGTTCG 1548	1309 CCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGN 1368

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201 CICHAIGSASACCATATACIA HARIGAGAGGICCCTTAIGAIGCCAICAICAICAG 343 241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300	TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG	121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180 	61 TATAGATGGAAAACAAGCGACGAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120	1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTTCCTA 60	Simila 9; Cc	bacteraemia and/or pneumonia. The present sequence encodes the S. pneumoniae BVH-11 protein antigen. Sequence 2647 BP; 934 A; 538 C; 556 G; 619 T; 0 other;	antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otilis media,	The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein	Streptococcal antigens useful for vaccinating against e.g. meningitis, otitis media, bacteremia and/or pneumonia - Example 6; Fig 15; 106pp; English.	Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N; WPI; 2000-452397/39.	23-DEC-1998; 98US-0113800. (BIOC-) BIOCHEM PHARMA INC.	06-JUL-2000. 20-DEC-1999; 99WO-CA01218.	Streptococcus pneumoniae. WO200039299-A2.	Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal; ds.	21-NOV-2000 (first entry) Streptococcus pneumoniae BVH-11 gene SEQ ID NO:12.	55736 stan 55736;	RESULT 8 AAA65736	2299 GATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGCGTTGTTAAAAGGAAGTAA 2358
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1309 CCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGN 1368	1249 AAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGA	1189 TEATGETCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAAATCTTGAAAGCAAGTTATC		1139 TAGTCAGCTGCTAGGAAAATCTTGGGGAAGGAATGGAAT	GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGG	961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG	901 AGCTAGAGGTGTTGCAGTGCCACAGGAGATCATTACCACTTCATCCCTTACTCTCAAAT	841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAGCGAAGTCGAAGTCGAAGTCGAAGTCGAAGTCGAAGTCGAAGTCGACGAATCACAAGTCGAATCTGATGGCCTTATTTTCGACCCAGGGCAAATCACAAGTCGAAGTCGAAG	781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 	721 TGTAAGCAATCCAGGAACTACAAATACTAACACÁAGGAACAACAGCAACACACTAACAGTCA 	661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC	601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA	541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT	481 AGGACGCTATACTACAGATGATGGTTATATCŤTTAATGCTTCTGATATCATAGAGGATAC 	421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA	361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC	301 GSTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC	344 TGANGAGCTCCTCATGAAAGATCCGAATTATCAGTTGAAGGATTCAGACATTGTCAATGA

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GGACAACAATACTATTATGGCAGAAGCTGAAAAACTATTGGCTTTATTAAAGGAGAGTAA

Query Match Best Local Similarity Matches 1819; Conserv

Conservative

0,

Mismatches

539; DΒ 24;

102;

Gaps

2

57.5%; 73.9%;

Score 1374.2; Pred. No. 0;

Length

Sequence 2647

BP; 934 A; 538 C; 556 G; 619

T; 0 other

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RESULT 9
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                                                           The invention describes an isolated polypeptide (I) with 70-90% cidentity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II) CC comprising (I) is useful for therapeutic or prophylactic treatment of individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial cC infection (e.g., caused by Streptococcus proeumoniae, group A Streptococcus such as Streptococcus pyogenes, group B Streptococcus such as Streptococcus aureus) in an individual susceptible to the infection.

CC as polymucleotide (III) encoding (I) is useful in DNA immunisation at techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA cc probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be clasmostic griculating S. pneumonia nucleic acid in a sample for C diagnosing streptococcal infections. This sequence encodes the antigenic poptides described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components or preventing streptococcal infections such as otitis media
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/product= "BVH-11"
/note= "The gene is flanked by sequences from the
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                                       The DNA sequences can be used for producing an immune response to Streptococcus pneumoniae in a mammal. Antibodies against the protein can be used to inhibit S. pneumoniae-mediated C3 degradation. C3-mediated inflammation and rejection in xenotransplantation can be inhibited by expressing the nucleic acid sequences on the surface of organ of an animal. In particular, the polypeptides are useful for stimulating the immune system and are effective to immunize or treat mammalian subject against Streptococcus pneumoniae infection or
                                                                                                                                                             The present sequence, isolated from Streptococcus pneumoniae, enchuman C3-degrading protein (see AAY91939) of about 92 kDa. This sequence may encompass a smaller 20 kDa polypeptide coding sequence may encompass a C3-degrading activity.
                                                                                                                                                                                                                                      Claim
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31-MAR-1999;
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AMERICAN CYANAMID
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                                                                                                                                   ATCAGAACGCCATGTGGAATCTGATGGCCTTATTTTCGACCCAGCGCAAATCACAAGTCG
                                                                                                                                                          GAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCG
                                                                                                                                                                                                                                                     GATTGTCAGAGAACCACAATCT-----
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                  AATGTCTGAATTGGAAAAACGAATTGCTCGTATTATTCCCCCTTCGTTATCGTTCAAACCA
                                  AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA
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Pred. No. 4.6e-245;
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CAGTGAAGATCCAAATAAGAACTTCAAAGCGGATGA--
                                                                                                                                                                                           CTATACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACG
                                                                                                                                                                                                                                                                                                      TCATTACCATAATATTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGG
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                                                                                                                                                              CCATTACCATAACATCAAATTTGAGTGGTTTGACGAAGGCCTTTATGAGGCACCTAAGGG
                                                                                                                                                                                                                                                                                                                                                                             TTACAATCTTCAATATACTGTAGAAGTCAAAAACGGTAGTTTAATCATACCTCATTATGA
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                                                   TCCGCATTCAGATAATGGTTTTGGTAACGCTAGCGACCATGTTCAAAGAAACAAAATGG
                                                                                                   ATATATGGTTGAGCATACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCAGAAGCTATCTACAACCGCGTGAAAGCAGCTAAGAAGGTGCCACTTGATCGTATGCC
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                                               GGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGCGTTGTTAAAAGGAAGTAA
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                                                                                                      CAAGTCCAATGCCAAAGAGACTCTCACAGGATTAAAAAATAATTTACTATTTGGCACCCA
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AAA05417 standard; DNA;

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ARACULT 11
ARACUTT 12
ARACUTT 13
ARACUTT 13 Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antiinflammatory; meningitis; infection; diagnosis; pneumococcal disease; ds. Streptococcus 24-MAY-2000 (first pneumoniae nucleotide entry) sequence

Streptococcus pneumoniae

10-FEB-2000

27-JUL-1999; 99WO-GB02451

27-JUL-1998; 19-MAR-1999; 98GB-0016337. 99US-0125164.

(MICR-) MICROBIAL TECHNICS LTD

Gilbert CFG, Hansbro PM;

2000-195300/17.

New Streptococcal protein, pneumococcal diseases and or inhibiting expression o n, useful as a vaccine, for did of for screening agents capable of the protein for diagnosis of capable of antago antagonizing

Page 99; 108pp; English

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AAY81501 to AAY81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be used in vaccines and in diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection

18 AACCGCCAGAGGTGTAGCTGTCCCTCATGGTAACCATTACCACTTTATCCCCTTATGAACA 977	AACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCA	838 GAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCG 897	778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 837	718 TICTGTAAGCAATCCAGGAACTACAAATACTAACACAGGAACAACAGCAACAGCAACAG 777	658 AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717	598 GTTATCAGCTAGCGAGTTGGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 657	38 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597	78 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537	418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTC 477	358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC	98 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357	38 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA 297	178 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237	118 CAAGCGTGAAGGAATGATGGTGAGGAAATCGTCATGAAGATAACAGACCAAGGCTATGT 177	58 CTATATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG 117	1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTC 57	Y Match 42.0%; Score 1003.8; DB 21; Length 2481; Local Similarity 66.0%; Pred. No. 4.8e-243; hes 1623; Conservative 0; Mismatches 693; Indels 144; Gaps 6;	equence 2481 BP; 839 A; 514 C; 538 G; 590 T; 0 other;
2026	Qy 1966 CTATACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGACG 2025		1846 ATATATUGUTUGAGATACAGTTGAGGTTAAAAACGGTAATITGATTATTCICATAANGGA	100 TOLAGO AGUTATITACAN CONTRA NA CO	1786 TEGENGENGTTTACABTEGETERA BANGGERA BANGGERA BANGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTTCAGGETTCAGGETTCAGGETTCAGGETTTCAGGETTCAGGETTTCAGGETTCAGGETTCAGGETTTCAGGETTCAGGETTCAGGETTTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTCAGGETTC		1638 TGATATAACCAGTGATGAGGGGGATGCCTATGTAACTCCACATATGACCCATAGCCACTG	1576 TOTAL TOCK CANTING CONTROL TO THE TOTAL CONTROL TO THE TOTAL CONTROL TO THE TOTAL CONTROL TO THE TOTAL CONTROL CO	1486	1426 TGATGAATGGCATAATAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCCAAT	1306 ISWAAA FAAGGETOG AAT TO TAA I TOCAGOO I AGACAAA TA TAGAACGA TOAA	1338 TGATCGAGAATTTTACAATAAGGCTTATGACTTACTAGCAAGAATTCACCAAGATTTACT	1296 TICAMACHAGHGAGISII (ACACACIII INCLIGUI MAHAMAGHANAIGI GCICCIIGG			ہے دہ د	1018 TTGGCTACCAGATTCAAGGCCAGAACAACCAACTCAGACTCCGGAACCTAGTCC	

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            The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as
                                                                          Claim
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                                                                                                                                                                                                                                                                                                                         Streptococcus
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                                                                                                       proteins and nucleic acid molecules from Streptococcus pneumoniae, ful as medicaments for treating or preventing a disease or infection to streptococcus bacteria, such as pneumonia, sepsis, otitis media
                                                                                                                                                                                                                                                                                                                                                         infection;
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   included are an antibody
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                               CACGGGTGATGCTTATATCGTTCCTCACGGCGACCATTACCATTACATTCCTAAGAATGA
                                               TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA
                                                                       CCAAGGACGTTATACAACGGATGATGGGTATATCTTCAATGCATCTGATATCATTGAGGA
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CC proteins, treating a patient by administering the protein, DNA or CC antibody (in a composition), a kit comprising first and second primers, CC which are the nucleic acid cited above or fragments between nucleotides CC which are the nucleic acid cited above or fragments between nucleotides CC which are the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers of complementary to the complement of the target sequence, and where the parts of the primers CC having substantially complementary to the compound complement of the target sequence, and where the parts of the primers CC having substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound cc with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more CC protein and a Streptococcus pneumoniae bacterium, where one or more CC uncleic acid molecules, antibody and compositions are useful as CC streptococcus bacteria, particularly S. pneumoniae, such as pneumoniae, such as pneumoniae, occurrence, diagnostics and antibiotics. The methods are useful for contentified coding region from the present sequence is one of the 2489 identified or ear infection. They are also useful for the 2489 identified and antibiotics.
                                                                                                                                                           the 2489 identified coding region from the genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                              ftp.wipo.int/pub/published_pct_sequences.
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TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTC TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT CTATATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA CAGTCATAATCAT CAGTGAAGAGCTCCTCATGAAAGATCCGAATTATCAGTTGAAGGATTCAGACATTGTCAA GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTTCCTTATGATGCCATCAT TAAGAGGGAGGGGATCAACGCCGAACAAATTGTTATCAAGATTACGGATCAAGGTTATGT TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAACTTGACACCAGATGAAGTCAG TTCCTATGAGCTTGGACGTTACCAAGCTGGTCAGGATAAGAAGAGTCTAATCGAGTTGC TGCAGCTCATGCGGATAATATTCGGACAAAAGAAGAGATTAAACGTCAGAAGCAGGAACG TGAAATCAAGGGTGGTTATGTCATTAAGGTAAACGGTAAATACTATGTTTACCTTAAGGA TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA---TAATCGTGTTTC Conservative 41.6%; 0, Score 993; DB Pred. No. 2.6e-0; Mismatches - AACTCAAGAGCAGATAATGCTGTTGCTGCAGCCAGAGC .6e-240; 696; Indels 141; Gaps 417 119 57 537 530 477 419 357 359 297 237 239 177 179 299 σ

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RESULT 13
AAA47605
Streptococcus pneumoniae; infection; vaccine; coiled coil region; histidine triad residue; Sp36; antibody; otitis media; nasopharyngeal infection; bronchial infection; bronchitis; sepsis meningitis; lobar pneumonia; ds.
                                                                      Streptococcus
                                                                                                                                           Recombinant variant of Sp36 gene (Sp36B) of S. pneumoniae
                                                                                                                                                                  20-OCT-2000
                                                                                                                                                                                                         AAA47605
                                                                                                                                                                                                         standard;
                                                                                                                                                                  (first
                                                                      pneumoniae
                                                 Location/Qualifiers
                  product= Sp36B polypeptide
                             /*tag=
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine useful for prophylaxis and treatment of pnemococcal infections such as otitis media, nasopharyngeal and bronchial infections, comprises Streptococcus pneumoniae proteins
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TTCCTATGAACTTGGTCGTCACCAAGCTGGTCAGGTTAAGAAAAGAGTCTAATCGAGTTTC 119 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA----TAATCGTGTTTC

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CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as CC ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or CC antibody (in a composition), a kit comprising first and second primers, CC which are the nucleic acid cited above or fragments between nucleotides CB-100 of a sequence not defined in the specification, for amplifying a CC target sequence not defined in the specification, for amplifying a CC target sequence is substantially complementary to the target sequence, and where the parts of the target sequence, and where the parts of the target sequence, and where the parts of the target sequence to be amplified, assay comprising contacting a test compound CC with the protein, and determining whether the test compound CC with the protein, and determining whether the test compound CC genes encoding the proteins has been rendered inactive. The proteins, CC mucleic acid molecules, antibody and compositions are useful as CC medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis media or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for CC identifying immunodominant proteins. The present sequence is one of the 2489 identified codding region from the genomic sequence.

CC Note: The sequence data for this patent did not form part of the printed, specification, but was obtained in electronic
  Matches 1478;
                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or ear infection
                                                                                    Sequence 2517 BP; 830 A; 509 C; 545 G; 633 T;
                                                                                                                                                  of the printed specification, but format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Masignani V,
                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; SEQ ID No 1985; 56pp; English
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Pred. No. 1.5e-239;
Mismatches 636;
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1186 TCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTT 1245 	1126 GGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTC 1185	1078 AGGCCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTT 1125	1018 TIGGGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCC 1077	958 AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 1017 	898 AACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCA 957	838 GAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTTGATCCAGCACAAATCACAAGTCG 897	778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 837	718 TTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAGGAACACTAACAG 777	658 AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717	598 GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 657	538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597	478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537	418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTTGGCACGTTC 477	358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC	298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357	238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA 297	178 CACTTCACATGGCGACCACTATCATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237	180 TAAGAGGGAGGGATCAACGCCGAACAAATCGTCATCAAGATTACGGATCAAGGTTATGT 239
AC AAA47602; XX 20-OCT-2000 (first entry)	RESULT 15 AAA47602 ID AAA47602 standard; DNA; 2531 BP.	Db 2178 TGAATCTGATG 2188		2026 TCCACATTCTAATGATGGATGGGCAATGCCATGGCTGGTTAGGCAAGAAAGA	1986 CHALACCIUSAASATITSIIIGCGACGATTAAGTACTACGAACAACG	1906 TCATTACCATAATATTAAATTTGCTTGGTTTGATGATCACAAGCTCCAAATGG	1846 ATATATIGGTTGAGCATACAGTTGAGGTTAAAACGGTAATTTGATTATTCCTCATAAGGA	18	1726 AAAAAGTATCCTACCTCCATCTCCARCACGCAGATGTTAAACCAAATCCAACTGGAGATAG	QY 1666 GATTGGAAAGATAGCCTTTCTGATAAGAAAAAGTTGCAGCCTAAGCCTATACTAAAGA 1725	1606 TGATATPATCAGTGATGAAGGAGATGCATATGAACGCCTCATATGGGCCATATGCACTG	1546 TCGTATTGCTCAATTACCTGATAACAGTATACAGTCAGATGGATG	1486 TACCCATCCAGAGCGACTTGGCAAACCAAATTCAGTATAGTATACTCAGAGAGAG	14 14	1366 TGNAAATAAGGGTCGTAATTCTGAATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAA 	1338	1246 ATCAAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCG	

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae; infection; vaccine; coiled coil region; histidine triad residue; Sp36; antibody; otitis media; nasopharyngeal infection; bronchial infection; bronchitis; sepsis; meningitis; lobar pneumonia; ds.
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                    GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTCCCTTATGATGCCATCAT
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Best Local (
                                                                                                                                                  Matches 1478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or ear infection -
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                                                                                                                                                                                                                                                                                                                of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the
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                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
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(GENO-) INST GENOMIC RES
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                                                                                                                                                                        Similarity
CTATATAGATGGAAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG
                                                     TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA---TAATCGTGTTTC
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Pred. No. 2.8e-238;
0; Mismatches 636;
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                                                                                                                                                                                         Length 2162598;
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AAATCCÁGCTCÁACCÁAGÁTTGTCÁGÁGÁAACCÁCÁATCTGÁCTGTCÁCTCCAÁCTTÁTCA 838748
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                                                                                                                                 AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCCTTCGTTATCGTTCAAACCA 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACCAGCTCTACAAACTGCCTTT
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                TCGTTATATCCCCAGCCAAGGATCTTTCAGCAGAAACAGCAGCAGGCATTGATAGCAAACT 839225
                                           TCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTT
                                                                                       GGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTC 1185
                                                                                                                                                                                                                                                      AATGTCTGAATTGGAAAAACGAATTGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA
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                                                                           standard;
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Best Local
                                                                                                                                                                                                                       Matches 1481;
                                                                                                                                                                                                                                                                                                   The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protective or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid encoding antigenic peptide(s) from Streptococcus
iae - or their epitope-containing fragments, useful in
ive or therapeutic vaccines, and for diagnosis
                                                                                                                                                                                                                                    Similarity
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GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTTCCTTATGATGCCATCAT
                    CACTTCACATGGCGACCACTATCATTACTACCAATGGTAAGGTTCCTTATGACGCTATCAT
                                                                             CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT
                                                                                                          TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAACTTGACACCAGATGAAGTCAG
                                                                                                                                      CTATATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG
                                                                                                                                                                 Hromockyj A,
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/transl_except= (pos:1406..1408,aa:Xaa)
/transl_except= (pos:1430..1432,aa:Xaa)
/note= "no stop codon given; Xaa is unspecified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product= "SP0042"
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                                                                                                                                                                                                                                                                             766 A; 474 C; 498 G;
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67.7%;
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Pred. No. 5.7e-
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Streptococcus pneumoniae antigens, useful for detecting Streptococcus and for preventing or attenuating disease caustreptococcus infection -
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standard; DNA; 2639

21-NOV-2000 (first entry)

Streptococcus pneumoniae BVH-11-2 gene SEQ. ID NO:13

Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal; ds.

Streptococcus pneumoniae Ş

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcal antigens useful for vaccina otitis media, bacteremia and/or pneumonia
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                                                                                                                                                                                                                                                                                                            /product= "BVH-11-2"
/product= "The gene is flanked by sequences from the vector SP64, no information on which is
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus progenes, group B Streptococcus such as Streptococcus progenes, group B Streptococcus such as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia or staphylococcus aureus) in an individual susceptible to the infection. A polynucleotide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcus infections. This sequence encodes the Streptococcus pneumoniae protein BVH-11-2, used to create the antigenic peptides described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine comprising (I) is useful for therapeutic or prophylactic treatment omeningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                              CACGGGTGATGCTTATATCGTTCCTCACGGCGACCATTACCATTACATTCCTAAGAATGA
                                                                                                            CCAAGGACGTTATACAACGGATGATGGGTATATCTTCAATGCATCTGATATCATTGAGGA
                                                                                                                                            GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA
                                                                                                                                                                                                         TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTC
                                                                                                                                                                                                                                                                                                                       TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA
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                                                                           TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA
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Pred. No. 3.2e-237;
0; Mismatches 638;

    - AACTCAAGAGCAGATAATGCTGTTGCTGCAGCCAGAGC

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GATTAAAAAAGATAGTTTGTCTGAAGCTGAGAGAGCGGCAGCCCAGGCTTATGCTAAAGA
                               GATTGGAAAAGATAGCCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGA
                                                                                                                                   TGATATAATCAGTGAATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTG
                                                                                                                                                                                                                                      TCGTATTGCTCAATTAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACA
                                                                                                                                                                                                                                                                                                                                  TACCCATCCAGAGCGACTTGGCAAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGT
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                                                                                                TGATATAACCAGTGATGAGGGGGATGCCTATGTAACTCCACATATGACCCATAGCCACTG
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AAX25394 standard; DNA; ВP

19-JUL-1999 (first entry)

Streptococcus pneumoniae complement C3-degrading protease

Human complement C3-degrading protease; vaccine; infection; meningitis; pneumonia; xerotransplantation; transplant rejection; inflammation; ds.

Streptococcus pneumoniae

WO9915675-A1

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24-SEP-1998; 98WO-US20186

24-SEP-1997; 97US-0059907

AMERICAN CYANAMID CO UNIV MINNESOTA.

Cheng Q, Finkel DJ, Green BA,

Hostetter MK,

Masi

ΑW

WPI; 1999-254719/21. P-PSDB; AAY05753.

New isolated human complement C3-degrading proteinase

Claim 54; Page 52-54; 66pp; English

RESULT 21
AAX25394
ID AAX25
XX AAX25
AC AAX25
XX AAX25
XX Human
CX Human
CX Human
CX Strep
XX Mennir
XX WO991
XX Cheng
XX WPI,
DR WPI,
DR WPI,
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DR WPI,
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CC This
CC This This DNA sequence encodes a 79 kDa protein (see AAY05753) of Streptococcus pneumoniae serotype 4 that is capable of degrading human complement protein C3 (HCPC3). It was identified in the S.

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pneumoniae serotype 4 genome by alignment to another novel open creading frame (see AAX2533) that codes for a 20 kDa HCPC3 protease C (AAY05752) of S. pneumoniae serotype 3. This suggested the open reading frame that codes for the 20 kDa protein may be part of a clarger open reading frame. Amino acids 1-58 and 90-132 of the 20 kDa protein have substantial sequence identity with amino acids 170-227 and 258-300 of the 79 kDa protein. Proteins and peptides or polypeptides containing these regions, and DNA sequences encoding them (nucleotides 507-681 and 827-99) of the present sequence) are claimed. HCPC3 proteases and polypeptides can be used as immune system stimulating compositions (claimed). They can produce an amamalian subject against S. pneumoniae to immunize or treat a mammalian subject against infection or colonization (claimed). They can produce a B cell response, a T cell response, an epithelial cell response or an endothelial cell response (claimed). The expression of the proteins on the surface of an organ of an animal used in xenotransplantation can be used to inhibit C3-mediated inflammation and rejection.
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Best Local Simi
Matches 1436;
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Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1) to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1) to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1) to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1) to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1) to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1) to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1) to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1) to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1) to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1) to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1) to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1) to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1) to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1) to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1) to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1) to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1) to 391) where the streptococcus pneumoniae genome genom
                                                                               The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV5214 to AAV52524) recorded on it, or a representative fragment or a sequence at least identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from
                                                                                                                                                                                                                                                 Claim 1;
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nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the SEQ ID NO:1 to 391, identifying members of the collating the nucleic acid molecules from the members; or (b) isolating meNA, DNA or CDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
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Sequence 2359 BP; 786 A; 451 C; 511 G; 611 T; 0 other; 27.4%; Score 653.8; DB 19 Pred. No. 1.1e-154; 19; Length

CTATATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT TTATATAGATGGTGATCAGGCTGGTCAAAAGGCCAGAAAACTTGACACCAGATGAAGTCAG TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTTGCCTTTGGCACGTTC GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTTCCTTATGATGCCATCAT CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT TAAGAGGGAGGGGATCAACGCCGAACAAATTGTTATCAAGATTACGGATCAAGGTTATGT TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA---TAATCGTGTTTC AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC GTTATCAGCTAGCGAGTTAGCTGCTGCAGAAGCCTATTGGAATGG-------GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC CACGGGTGATGCTTATATCGTTCCTCACGGCGACCATTACCATTACATTCCTAAGAATGA CCAAGGACGTTATACAACGGATGATGGGTATATCTTCAATGCATCTGATATCATTGAGGA CAGTCATAATCATAACT TGCAGCTCATGCGGATAATTCCGGACAAAAGAAGAAGATTAAACGTCAGAAGCAGGAACG TGAAATCAAGGGTGGTTATGTCATTAAGGTAAACGGTAAATACTATGTTTACCTTAAGGA TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTTACCTTAAGGA CAGTGAAGAGCTCCTCATGAAAGATCCGAATTATCAGTTGAAGGATTCAGACATTGTCAA Conservative 0, Mismatches 413; - CAAGAGCAGATAATGCTGTTGCTGCAGCCAGAGC Indels 54: Gaps 1529 597 1238 177 117 1574 657 1469 1409 477 1358 1298 1178 1118 1058 57 717 357 297 998 ū

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The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence encodes the S. pneumoniae NEW12 protein antigen.

T; 0 other;

Score 548.4; DB 21; Pred. No. 5.3e-128; Indels Length 102; Gaps 2

GAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGAC CCGACTCCAGACCTAGTCCAAGTCCGCAACCTGCACCAAATCCTCAACCAGCTCCAAGC ccgactccggaacctagtccaggcccgcaacctgcaccaaatcttaaaatagactcaa--CTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAA GGTTATATCTTTGATCCTCGTGATATAACCAGTGATGAGGGGGGATGCCTATGTAACTCCA GGTTACATTTTTGATGAACATGATATAATCAGTGATGAAGGAGATGCATATGTAACGCCT GAGTATACTGAAGACGAAGTTCGTATTGCTCAATTAGCTGATAAGTATACAACGTCAGAT TTGGCATTCCTAGCACCAATTACCCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATT **AACCTGTTGGAACGACTCAAGGATGTCTCAAGTGATAAAGTCAAGTTAGTGGATGATATT** AAATTATTAGAACGCTTGAATGAATGAATCGACTAATAAAGAAAAATTGGTAGATGATTTA 1465 AGAATTCACCAAGATTTACTTGATAATAAAGGTCGACAAGTTGATTTTGAGGCTTTGGAT AAAACTGACCTCCCATCTAGTGATCGAGAATTTTACAATAAGGCTTATGACTTACTAGCA AAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACT GCAGGCATTGATAGCAAACTGGCCAAGCAGGAAAGTTTATCTCATAAGCTAGGAGCTAAG AAAAATCTTGAAAAGCAAGTTATCAAAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAA TTTGAGGAGAATGGAGTTTCTCGTTATATCCCCAGCCAAGAATCTTTCAGCAGAAACAGCA TTCGAAGAAAAGGCCATCTCTCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTT AATCCAATTGATGAGAAATTGGTCAAAGAAGCTGTTCGAAAAGTAGGCGATGGTTATGTC -----ATTCTTTGGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTA CTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAGACCAGAAGAACCAAGTCCACAA 2067 1705 2367 1645 2307 1585 2247 1525 2187 2127 1405 2007 1947 1225 1827 1115 1767 1057 1285 1887 1165

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                                                                                                                                            Streptococcus pneumoniae; antigen; vaccine; infedetection; pneumonia; otitis media; meningitis;
                                                                                                                                                                                                                   Streptococcus pneumoniae SP103 nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a protein from Streptococcus pneumoniae.

The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their callelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 631; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                        ATACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGGAAAT 396
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                                                                                                                                                                                                                                                                                                            AGTTCCTTATGATGCCCTCTTTAGTGAAGAACTCTTGATGAAGGATCCAAACTATCAACT
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756 672 696 636 555 576

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1342; 60;

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Query Match Best Local Similarity 65.3%; E	CC bacteraemia and/or pneumonia. The pre CC S. pneumoniae BVH-3A protein antigen. XX SQ Sequence 1455 BP; 491 A; 286 C; 285 G	gens, may be used for encode. The protein a intion and treatment of cially humans) which	present invention desc pens (II) from Strepto bactericidal activity	s media, bacteremia a cosure; Fig 7; 106pp;)B; AAB127)tococcal	2000-452397/39.	:-) BIOCHEM PHARMA INC.	23-DEC-1998; 98US-0113800.	20-DEC-1999; 99WO-CA01218.	06-JUL-2000.	WO200039299-A2.	stococcus pneumoniae lylaxis; therapy; ini s media; pneumonia;	otococcus pneumoniae	AAA65733; 21-NOV-2000 (first entry)	733 standard; DNA; 1455	SULT 26 165733	997 CCTTCGT 1003	937 CCACTICATCCCTTACTCTC/ 	877 TCCAGCACAAATCACAAGTCO	817 ACAGCTCTACAAACTGCCTTT	Qy 757 CAACAACAGCAACACTAACAC	673
Score 385.4; DB 21; Length 1455; Pred. No. 5.5e-87;	The present sequence encodes the antigen. C; 285 G; 393 T; 0 other;	broduction of be used as valued in infections in neningitis, otherwise.	ribes nucleic acids (I) encoding protein scoccus pneumoniae. The protein antigens 1.7. The nucleic acids, encoding the protein 1.7.	pneumonia - 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	for vaccinating against e.g. meningitis,	1, Martin D, Rioux C, Charland N;						; BYH-3; BYH-11; BYH-28; antigen; vaccine; fection; diagnosis; meningitis; bacteraemia; immunisation; bactericidal; ds.	gene SEQ ID NO:7		89.			CCACTTCATCCCTTACTCTCAAATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCC 996	TCCAGCACAAATCACAAGTCGAACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTA 936	ACAGCTCTACAAACTGCCTTTGAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGA 876	CAACAACAGCAACACTAACAGTCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAA 816	TAACACGCAATCTGT 687
RESULT 27 AAA47603	Db Qy	Db Qy	Db X	S B ;	OV Db	Q	Db .	Q E	P 8	Db	8	Qy Db	Db	Db	Ş.	Qy Db	Db Qy	Qy Db	Qy Db	Db Qy	Qy Db	Matches
7	997 CCTTCGT 1003 	937 CCACTTCATCCCTTACTCTCCAATGCTCTAATTGCAAACGAATGCTCCTATTATTCC	9 .	9	759 AGCAĀĀAGGATCAACTĀGCĀAGĆCĀĞCĀĀATĀĀĀTCTGĀAĀĀTCTCCAĞĀĞTCTTTTGĀĀ 817 ACAGCTCTĀCAĀACTGCCTTTGĀGTCAACGĀCATGTĀGĀATCTGĀTGGCCTTGTCTTTGĀ	757 CAACAACAGCAACACTAACAGTCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTTGAA	4	٠ ,	637 ATCTGGTCGAGGAAATCTGTCAAATTCAAGAACCTATGGCCGACAAAATAGCGATAACAC 	7	577 CCATTACATTCCTAAGAATGAGTTATCAGCTAGCGAGTTGGCTGCTGCTGCTGCTGCTTCCT	517 TGCTTCTGATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTA	457 TGCTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGATGTTTATCTTTAA	9	7	337 ATACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAAT	277 AAAAGATGAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAA	217 GGTTCCTTATGACGCTATCATCAGTGAAGATTACTCATGAAGATCCAAACTATAAGCT 	157 GATAACAGACCAAGGCTATGTCACTTCACATGGCGACCACTATCATTACTACAATGGTAA 	97 TITGACTCCTGATGAGGTTAGCAAGCGTGAAGGAATCATCAATGCTGAGCAAATCGTCATCAA	37 TAAGGAAAATAATCGTGTTTCCTATATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAA	s 631; Conservative 0; Mismatches 276; Indels 60; Gaps

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Matches 631
                                                                                                                                                                                                                                                                  polypeptides in vaccines to protect against a wide variety of S. pneumoniae. New vaccine compositions are described which comprise streptococcus pneumoniae polypeptide (or fragments) of 80 . Amino acids in length that comprise at least one histidine triad residue (HxxHxH) or a coiled-coil region, or an antibody directed against these features. The vaccine is useful in protecting against infection by Streptococcus pneumoniae. The vaccine composition comprising antibodies to is useful for passive immunization for treating pneumococcal infections which includes otitis media, nasopharyngeal
                                                                                                                                                                                                                                                                                                                                                                                              Although a number of proteins have been suggested as being involved in the pathogenicity of Streptococcus pneumoniae, there still remains a need to identify polypeptides having epitopes in common from various strains of S. pneumoniae in order to utilise such
                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine useful for prophylaxis and treatment of pnemococcal infections such as otitis media, nasopharyngeal and bronchial infections,
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                                                      CTTGACACCAGACCAGGTTAGCCAGAAAGAAAGGAATTCAGGCTGAGCAAATTGTAATCAA
                                                                        TTTGACTCCTGATGAGGTTAGCAAGGGTGAAGGAATCAATGCTGAGCAAATCGTCATCAA
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY81501 to AAY81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be used in vaccines and in diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and maningitis. AAA05591 to AAA05591 represent primers used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcal protein, useful as a vaccine, pneumococcal diseases and for screening agents or inhibiting expression of the protein -
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                                                                                                                                          TCACTACATTCCCAAAAGCGATTTATCTGCTAGTGAATTAGCAGCAGCTAAAGCACATCT
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TTCAAGAACAAACTGGGTACCTTCTGTAAGCAATCCAGGAACTACAAATACTAACAAAG
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identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), aki comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New proteins and nucleic acid molecules from Streptococcus useful as medicaments for treating or preventing a disease due to streptococcus bacteria, such as pneumonia, sepsis, o or ear infection
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CC Note: The sequence data for this patent did not form part confidence in the printed specification, but was obtained in electronic confidence in the proteins of the printing from WIPO at the confidence in the proteins of the printing from WIPO at the printing from WIPO at the proteins of the protein was obtained in electronic confidence.
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Pred. No. 7.7e-87;
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Query Match Best Local Similarity

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Score 385.4; DB 21; Length 3120; Pred. No. 7.7e-87;

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                                                                      The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence encodes the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 200
P-PSDB;
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Best Local Similarity
Matches 631; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes nucleic acids (1) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence encodes the S. pneumoniae BVH-3 protein antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                          ATATTATGTCTACCTGAAAGATGCAGCTCATGCTGATAATGTTCGAACTAAAGATGAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK15101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK15101 standard; DNA; 5048
20-JUN-2000; 2000US-212683P
                                                       19-JUN-2001; 2001WO-CA00908
                                                                                                                                                                               WO200198334-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pneumonia; streptococcal bacterial infection; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BVH-11; vaccine; meningitis; otitis media; bacteraemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATCAGT 2781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAACTCTATGATTCACCTAGCGCCCAACGTTACAGTGAATCAGATGGCCTGGTCTTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae BVH-3 version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                               /product= "BVH-3"
/note= "The gene :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1003
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                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                 "The gene is flanked by sequences vector SP64, no information on wh given in the specification"
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XX (SHIR-) SHIRE BIOCHEM INC.

XX Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;

XX WFI; 2002-12272/16.

DR WFJ; 2002-12272/16.

PPSDB; AAU75932.

XX New Streptococcus pneumoniae BWH-3 and BWH-11 variant and epitope-bearing streptococcus infections such as otitis media.

PT meningitis, and bacteraemia -

XX Example 3; Fig 2; 113pp; English.

XX The invention describes an isolated polypeptide (I) with 70-90% cidentity to Streptococcus pneumonia protein BWH-3, BWH-11, variants of the invention describes an isolated polypeptide (I) with 70-90% cidentity to Streptococcus pneumonia protein BWH-3, BWH-11, variants of BWH-3 or BWH-11, or chimeric sequences derived from them. A vaccine (II) comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcus buch streptococcus such as Streptococcus pneumoniae, group A streptococcus such as Streptococcus pneumoniae, S. dysgalactiae, group B Streptococcus such as Streptococcus pneumoniae, S. dysgalactiae, group B Streptococcus such as Streptococcus pneumoniae infection. (III) is useful in DMA immunisation content for the preumoniae and streptococcus in a biological sample for S. pneumoniae infection. (III) is useful in a biological sample for containing the bacteria. The DMA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for C diagnosing streptococcus pneumoniae protein BWH-3, used to create the antigenic peptides described in the method of the invention.
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밁 S 문 Ş 밁 Ş 밁 Ş 뫄 Ś 밁 δ 밁 á Matches Query Match Best Local Sequence 5048 BP; 1709 A; 907 C; 1104 G; 1328 T; 0 other; local Similarity 2235 2175 2115 2055 1995 1875 1935 457 397 337 277 217 631; 97 37 GATAACAGACCAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAA TITGACTCCTGATGAGGTTAGCAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAA 156 TAAGGAAAATAATCGTGTTTCCTATATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAA TGCTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGATGTTATATCTTTAA CAATCGTCAAAAACAAGAACATGTCAAAGATAATGAGAAGGTTA---CAATCGACAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGG ATATTATGTCTACCTGAAAGATGCAGCTCATGCTGATAATGTTCGAACTAAAGATGAAAT TAAAGACGCTGATATTGTCAATGAAGTCAAGGGTTGTTATATCATCAAGGTCGATGGAAA AAAAGATGAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAA 336 AGTTCCTTATGATGCCCTCTTTAGTGAAGAACTCTTGATGAAGGATCCAAACTATCAACT GGTTCCTTATGACGCTATCATCAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCT **AATTACAGATCAGGGCTATGTAACGTCACACGGTGACCACTATCATTACTATAATGGGAA** CTTGACACCAGACCAGGTTAGCCAGAAAGAAGGAATTCAGGCTGAGCAAATTGTAATCAA TAAGGACAATAATCGTGTCTTCTTATGTGGATGGCAGCCAGTCAAGTCAGAAAAGTGAAAA ATACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAAAT Conservative 16.1%; 0 Score 385.4; DB 24; Pred. No. 9.5e-87; Mismatches 276; Indels Length 60; -----ACTC 2282 Gaps 516 456 2234 2174 2114 276 2054 216 1934 1994 96

TAATGTTGCTGTAGCAAGGTCTCAGGGACGATATACGACAAATGATGGTTATGTCTTTAA

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                        Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                   07-MAY-1998
                                                                                                                                                                                                                                                                    Streptococcus
                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae; computer readable medium;
                                                                                                                                                                                         30-OCT-1997;
                                                                                                                                                                                                                                            WO9818931-A2
                                                                                                                                                                                                                                                                                                                                                          23-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                            AAV52325 standard; DNA; 6867 BP
              pneumoniae
                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
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                                                                                                   Choi GH,
Rosen CA;
                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                pneumoniae
                                                                                                                                                                                                                                                                    pneumoniae
                                                                                                                                                                96US-0029960
                                                                                                                                                                                          97WO-US19588
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                                                                                                                Dillon PJ,
                                                                                                                                                                                                                                                                                                                                genome
                                                                                                                                                                                                                                                                                          S. pneumoniae; genome; diagnosis; assay;
                                                                                                                                                                                                                                                                                                                                fragment SEQ ID NO:192
                                                                                                              Dougherty
                                                                                                               BA,
                       Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TAACACGCAATCTGT
                                                                                                               Fannon
                                                                                                               Z
                                      assays,
                                       and
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Claim 1; Page 1157-1161; 1409pp; English.

The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391 (AAV52524) are genomic fragments from streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.

Sequence 6867 BP; 1896 A; 1325 C; 1212 G; 2433 T; 1 other;

Query Match Best Local Similarity

16.1%; 65.3%;

Score 385.4; DB 19; Pred. No. 1.1e-86;

Length

Matches 6387 6567 6687 6219 6279 6327 6447 6507 6627 457 397 157 637 517 337 277 217 631; 37 97 ATCTGGTCGAGGAAATCTGTCAAATTCAAGAACCTATCGCCGACAAAATAGCGATAACAC ATACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAAGAGAGAAAT GGTTCCTTATGACGCTATCATCAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCT AATTACAGATCAGGGCTATGTAACGTCACACGGTGACCACTATCATTACTATAATGGGAA GATAACAGACCAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAA TTTGACTCCTGATGAGGTTAGCAAGCGTGAAGGAATCCAATGCTGAGCAAATCGTCATCAA TAAGGACAATAATCGTGTCTTTATGTGGATGGCAGCCAGTCAAGTCAGAAAAGTGAAAA TAAGGAAAATAATCGTGTTTCCTATATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAA TCACTACATTCCCAAAAGCGATTTATCTGCTAGTGAATTAGCAGCAGCTAAAGCACATCT CCATTACATTCCTAAGAATGAGTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCT TAAAGACGCTGATATTGTCAATGAAGTCAAGGGTGGTTATATCATCAAGGTCGATGGAAA AAAAGATGAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAA AGTTCCTTATGATGCCCTCTTTAGTGAAGAACTCTTGATGAAGGATCCAAACTATCAACT CTTGACACCAGACCAGGTTAGCCAGAAAGAAGGAATTCAGGCTGAGCAAATTGTAATCAA TCCAGCTGATATTATCGAAGATACGGGTAAATGCTTATATCGTTCCTCATGGAGGTCACTA TGCTTCTGATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTA 576 TAATGTTGCTGTAGCAAGGTCTCAGGGACGATATACGACAAATGATGGTTATGTCTTTAA TGCTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTTTAA CAATCGTCAAAAACAAGAACATGTCAAAGATAATGAGAAGGTTA---CAATCGACAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGG ATATTATGTCTACCTGAAAGATGCAGCTCATGCTGATAATGTTCGAACTAAAGATGAAAT Conservative 0 Mismatches 276; Indels -----ACTC 60; Gaps 6628 696 6220 396 6100 636 6160 516 6280 456 6328 6388 336 6448 6508 216 156 96 276 6568 N

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RESULT 35
AAV524488
ID AAV524488
AC AAV52
AC AAV
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Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                    Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) scr
                                                                                                                              The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAVS2134 to AAVS2524) recorded on it, or a representative fragment or a sequence at least identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted is SEQ ID NO: 1 to 391 (AAVS2134 to AAVS2524) are genomic fragments from SEQ ID NO: 1 to 391 (AAVS2134 to AAVS2524) are genomic fragments from
                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 1369-1370; 1409pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
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vaccine; pharmaceutical composition;
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RESULT 36
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AAA65738

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GTTATCAGCTAGCGAGTTAGCTGCTGCAGAAGCCT

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Best Local S
Matches 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence an isolating the nucleic acid molecules from the members; or (b) isolating mcNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
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                                             CACGGGTGATGCTTATATCGTTCCTCACGGCGACCATTACCATTACATTCCTAAGAATGA
                                                              TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA
                                                                                                          CCAAGGACGTTATACAACGGATGATGGGTATATCTTCAATGCATCTGATATCATTGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence encodes the S. pneumoniae SP63 BVH-3 protein antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 6; Fig 18; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcal otitis media,
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infection; diagnosis; meningitis; bacteraemia;
ia; immunisation; bactericidal; ds.
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The invention describes an isolated polypeptide (I) with 70-90% (I dentity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II) CC comprising (I) is useful for therapeutic or prophic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection CC in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcual bacterial CC infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus propens, group B Streptococcus Streptococcus aureus) in an individual susceptible to the infection. CC A polynucleotide (III) encoding (I) is useful in DNA immunisation CC techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA CC probes for use in detecting the presence of Streptococcus in a biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media, meningitis, and bacteraemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 8; Fig 9; 113pp; English.
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RESULT 38
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Best Local
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WO200017370-A1
                              Streptococcus pneumoniae
                                                             Human C3-degrading protein; inhibitor; inflammation; or;
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                                                                                                                                                 19-JUL-2000
                                                                                                                                                                                  AAA08556
                                                                                                                                                                                                                 AAA08556 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2528 BP;
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                                                                                                                                                                                                                                                                                                   GGCTGGAAAAAATATGCAACCGAGTCAGTTAAGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCTTCTGATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAATCGACAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGG
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                                                                                                                                                                                                                 DNA;
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73.0%;
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                                                                 organ
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                                                               kDa; immunostimulatory; rejection; xenotransplar
                                                                                                               protein
                                                                 xenotransplantation;
                                                                                                                                                                                                                                                                                                   663
                                                                                                               coding
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence, isolated from Streptococcus pneumoniae, encodes a human C3-degrading protein (see AAY91938) of about 20 kDa. This sequence may be part of a larger open reading frame (see AAA0857) which encodes an approximately 92 kDa protein also having human C3-degrading activity. The DNA sequences can be used for producing an immune response to Streptococcus pneumoniae in a mammal. Antibodies against the proteins can be used to inhibit S. pneumoniae-mediated C3 degradation. C3-mediated inflammation and rejection in xenotransplantation can be inhibited by expressing the nucleic acid sequences on the surface of an organ of an animal. In particular, the polypeptides are useful for stimulating the immune system and are effective to immunize or treat a mammalian subject against Streptococcus pneumoniae infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MINU )
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31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colonization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 53; 63pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polypeptide is used to stimulate immune system and immunize treat a mammalian subject against Streptococcus pneumoniae infection
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DB; AAY91938.
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AMERICAN CYANAM
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                                                                                                                                                          TCTTTGGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGC
                                                                                                                                                                                                                                                                                                                                                       TCTCAAATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCCTTCGTTATCGTTCA 1012
                                                                                                                                                                                                                                                                                                                                                                                                  AGTCGAACCGCCAATGGTGTTGCTGTACCGCACGGAGACCATTATCACTTTATTCCTTAT
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                           AAGTTATCAAAACAAGAGAGTGTTTCACACA 1271
                                                                  GTTCCTCGTTATATCCCAGCCAAGGATCTTTCAGCAGAAACAGCAGCAGCAGCATTGATAGC
                                                                                          ATCTCTCGTTATGTCTTTGCGAAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGC 1240
                                                                                                                                  AAATTGGTCAAAGAAGCTGTTCGAAAAGTAGGCGATGGTTATGTCTTTGAGGAGAATGGA
                                                                                                                                                                                                                    AGTCCAGGCCGCAACCTGCACCAAATCTTAAAATAGACTCAA------ATTCT 1120
                                                                                                                                                                                                                                                                                                  AACCATTGGGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCT
 AAACTGGCCAAGCAGGAAAGTTTATCTCATA
                                                                                                                                                                                                   AACCATTGGGTACCAGATTCAAGACCAGAACCAAGTCCACAATCGACTCCGGAACCT
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99US-0283094.
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Pred. No. 2.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                   Sequence 1684 BP; 593 A; 292 C; 345 G; 453 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                          mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1284-1285; 1409pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barash
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae. The present invention also describes an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating
   1689 ATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACCTCCATCTC 1748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA,
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                                                                                                                               ATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAGCCTTTCTG
                                                                 ATGCCTATGTAACTCCACATATGACCCATAGCCACTGGATTAAAAAAGATAGTTTGTCTG
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Streptococcus pyogenes
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24-NOV-2000;
07-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds t (I). A composition comprising (I) or a nucleic acid encoding (I), may used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity cohromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus posens), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71556 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by
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       The sequence encodes Streptococcus pyogenes Group A Streptococci protein 36, GAS36. A recombinant cell producing GAS36, GAS36(2) or GBS36 is useful as a vaccine for vaccinating an animal, preferably a human against infection by a bacterial organism such as a streptococcal or staphylococcal bacteria, and for treating a disease caused by group A streptococci, group B streptococci or Staphylococcus aureus in an animal preferably a human. Vaccines and antibodies against the proteins of the invention are useful in prophylaxis and/or treatment of diseases such as necrotising fascilitis, scarlet fever, sepsis, impetigo, bacterial meningitis, otitis media, community-acquired pneumonia and many diseases
meningitis, of newborns.
                                                                                                                                                                                     New polypeptides obtained from group A or B streptococci , especi
Staphylococcus aureus homologous to Sp36 protein of Streptococcus
pneumoniae useful as antibacterial vaccines -
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         Group B Streptococcus; Streptococcus agalactiae; protein vaccine; screening; immunogen; detection; diagnosis; infe antibody; affibody; antibacterial; ds.
                                                   Group
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in AAY91275 to AAY91343) isolated from Group B Streptococcus (GBS),
known as Streptococcus agalactiae. The GBS polynucleotides and
polypeptides have antibacterial activity. Immunogenic compositions
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24-NOV-2000;
07-MAR-2001;
the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus; GAS
group A streptococ
antiinflammatory;
                                                                                                                                                                                                The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the tracters of the control of the 
                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 3860-3861; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2466 BP; 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus/GBS alactiae) or group A streptococcus/GBS (Streptococcus applactiae) or group A streptococcus/GBS (Streptococcus page one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7;
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Tettelin H;
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24-NOV-2000; 2000GB-0028727
07-MAR-2001; 2001GB-0005640
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TGAAATCTTAGACGGTTACGTTATTAAAGTCAATGGCAACTATTATGTTTACCTCAAGCC
                              TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357
                                                                                                                                  TACCTCACACGGTGACCATTATCATTTTACAATGGGAAAGTTCCTTATGATGCGATTAT
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        AAA05803 to AAA05872 encode proteins, polypeptides and peptides (given in AAY91275 to AAY91343) isolated from Group B Streptococcus (GBS), als Known as Streptococcus agalactiae. The GBS polynucleotides and polypeptides have antibacterial activity. Immunogenic compositions comprising GBS polynucleotides or polypeptides can be used as vaccines and for the treatment or prophylaxis of GBS infection. The polynucleotides and polypeptides can also be used in the detection of G and for screening DNA encoding bacterial cell envelope associated or screened antigens in gram positive bacteria. AAA05873 to AAA05941 represent primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Group B Streptococcus; Streptococcus agalactiae; protein antigen; vaccine; screening; immunogen; detection; diagnosis; infection;
                                                                                                                                                                  Claim 4;
                                                                                                                                                                                          New Group B Streptococcus
Streptococcal infections a
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence encodes Streptococcus agalactiae Group B Streptococci protein 36, GBS36. A recombinant cell producing GAS36, GAS36(2) or GBS36 is useful as a vaccine for vaccinating an animal, preferably a human against infection by a bacterial organism such as a streptococcal or staphylococcal bacteria, and for treating a disease caused by group A streptococci, group B streptococci or Staphylococcus aureus in an animal preferably a human. Vaccines and antibodies against the proteins of the invention are useful in prophylaxis and/or treatment of diseases such as mecrotising fasciitis, scarlet fever, sepsis, impetigo, bacterial meningifis, otitis media, community-acquired pneumonia and many diseases of newborns. The proteins are also used as immunogens to stimulate the production of antibodies for use in passive immunotherapy, for use as diagnostic reagents and for use as reagents in other processes such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptides obtained from group A or B streptococci , especially Staphylococcus aureus homologous to Sp36 protein of Streptococcus pneumoniae useful as antibacterial vaccines -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                  TAGTGAAGAGTTGTTGATGACGGATCCTAATTACCATTTTAAACAATCAGACGTTATCAA
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                                                             TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357
                                                                                                                                                                                                                    CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA
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                      AGGTAGTAAGCGCAAAAACATTCGAACCAAACAACAACTTGCTGAGCAAGTAGCCAAAGG
                                                                                                                                                                                                                                                                                                                                         TGCTGAAGAAGGCATCTCTGCTGAACAGATCGTAGTCAAAATTACTGACCAAGGTTATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        New Streptococcus protein for the treatment or prevention of inf
or disease caused by Streptococcus bacteria, such as meningitis,
for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-OCT-2000; 2000GB-0026333
24-NOV-2000; 2000GB-0028727
07-MAR-2001; 2001GB-0005640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus; GAS; GBS; group A streptococcus; Strept antiinflammatory; infection;
     the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. aggalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds (I). A composition comprising (I) or a nucleic acid encoding (I), may used as a vaccine or diagnostic composition. The disease caused by
                                                                                                                                                               The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus progenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for
                                                                                                                                                                                                                                                                                                                                                          Claim
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BVH-71

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Streptococcus pneumoniae; BVH-3; prophylaxis; therapy; infection;

BVH-11; BVH-28; antigen; vaccine; diagnosis; meningitis; bacteraemia;

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Matches 400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2469 BP; 842 A; 481 C; 519 G; 627 T; 0 other;
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TGGTGCTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTT
                          AACTAAAGAAGCTAAAGAAAAAGGTTTAGCTCAAGTGGCCCATCTCAGTAAAGAAGAAGT
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                                                                                                   TGAAATCTTAGACGGTTACGTTATTAAAGTCAATGGCAACTATTATGTTTACCTCAAGCC
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                                      Boyer M,
Rioux C;
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WPI; 1999-540309/45.
P-PSDB; AAY27346, AAY27347, AAY27348, AAY27349, AAY27350, AAY27351,
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                                                                                                 BIOCHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus; GBS; antigen; vaccine; Streptococcus infection; meningitis; pneumonia; immunocompromise; diabetes; liver disea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vetinary; mastitis;
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                                                               Charlebois I,
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(2716..2946)
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                                                                  Martin
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Matches 399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The GBS antigens can be recombinantly expressed using standard recombinant methodology. The GBS antigens of the invention can be used as vaccine components for the treatment or prophylaxis of diseases and symptoms mediated by Streptococcus infection, especially group A Streptococcus (S. pyogenes), GBS or S. agalactiae, S. dysgalactiae, S. uberis, S. nocardia, as well as Staphylococcus aureus. The vaccines are administered to those individuals at risk of GBS infection, particularly pregnant women and infants for sepsis, meningitis, and pneumonia, as well as immunocompromised individuals, such as those with diabetes, liver disease or cancer. The vaccines also have vetinary applications, such as for the treatment of mastitis in cattle. The present sequence represents a DNA encoding 8 GBS antigens of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5215 BP; 1631 A; 957 C; 1038 G; 1589 T; 0 other;
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                            TTACCATTACATTCCTAAGAATGAGTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTT
                                                                                                             TAATGCTTCTGATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                provides Group B Streptococcus (GBS) antigens and nucleic acids (AAX91103-X91111) encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus antigens - useful as vaccine for prophylaxis or therapy of Streptococcus infections
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Pred. No. 2.1
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RESULT 50
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Best Local S
Matches 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence encodes the S. pneumoniae GAS BVH-71 protein antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcal antigens useful for vaccinating against e.g. meningitis, otitis media, bacteremia and/or pneumonia - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA
                                         GACCTCACACGGTGACCATTATCATTTTTACAATGGGAAAGTTCCTTATGATGCGATTAT
                                                                              CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT
                                                                                                                          TGCTGAAGAAGCATCTCTGCTGAACAGATCGTAGTCAAAATTACTGACCAAGGTTATGT
                                                                                                                                                                                                        AGATGGAAAACAAGCGACGCAAAAA-----ACGGAGAATTTGACTCCTGATGAGGTTAG
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                                                                                                                                                             CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT
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nilarity 60.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             846 A; 480 C;
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immunisation; bactericidal; ds.
                                                                                                                                                                                                                                                                                                                                                                          Score 206.6; DB 2
Pred. No. 9.8e-42;
0; Mismatches 234
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Search co Job time	Dъ	γQ	Db	γQ	φ	γQ	Db	γO	Db .	γ	Db	γQ	Db	VΩ	dd
Search completed: November 13, 2003, 21:21:13 Job time : 726 secs	726 C 726	634 C 634	666 CTATCATTATATTCCTAAAAAAGATTTGTCTCCAAGTGAGCTAGCT	574 TTACCATTACATTCCTAAGAATGAGTTATCAGCTAGCGAGTTGGCTGCAGAAGCCTT	606 TAGTCCGACAGATATCATTGATGATTTAGGAGACGCTTATTTAGTACCTCATGGTAATCA	514 TAATGCTTCTGATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCA	546 TGCGGCAGTCAATGAAGCAAAAAAGACACGCTATACTACAGACGATGGCTATATTTT	454 TGGTGCTGTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTT	486 AACTAAAGAAGCTAAAGAAAAAGGTTTAGCTCAAGTGGCCCATCTCAGTAAAGAAGAAGAAG	418 TAGTCAACATCGTGAAG	426 AGGTAGTAAGCGCAAAAACATTCGAACCAAACAACAAATTGCTGAGCAAGTAGCCAAAGG	358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC	366 TGAAATCTTAGACGGTTACGTTATTAAAGTCAATGGCAACTATTATGTTTACCTCAAGCC	298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTTAAGGA	306 TAGTGAAGAGTTGTTGATGACGGATCCTAATTACCATTTTAAACAATCAGACGTTATCAA
			TAGCTGCTGCACAAGCTTA 725	TTGGCTGCTGCAGAAGCCTT 633	TTAGTACCTCATGGTAATCA 665	ATCGTTCCTCATGGAGATCA 573	ACAGACGATGGCTATATTTT 605	ACAGATGATGGTTATATCTT 513	CATCTCAGTAAAGAAGAAGT 545	-GTGGAACTCCAAGAAACGA 453	SCTGAGCAAGTAGCCAAAGG 485	NATCGACAAAAACAAGAGCA 417	TATTATGTTTACCTCAAGCC 425	TACTATGTTTACCTTAAGGA 357	

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ENTTS83TF Entamoeba histolytica (
genomic, genomic survey sequence.
BH153606
                                                                                                                                                                                                  Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                      Clones are derived from
                                                                                                                                                                                                                             Contact: Brendan J Loftus
                                                                                                                                                                                                                                                   Loftus, B., Wang, Z., Van Aken, S. and F
Determination of clone end sequences
                                                                                                                                                                                                                                                                  Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 906)
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Entamoeba histolytica
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                                                                                                                                                              DNA library
                                                                                                                                                                             Email: bjloftus@tigr.org
                                                                                                                                                                                                                                    Unpublished
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/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_l: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
                                                                                       /mol_type="genomic
/strain="HM1:IMSS"
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Sequencing: A Practical Approach, eds. M. Vaudin
Barell, Oxford University Press, 1999)."
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Eukaryota; Entamoebidae; 1 (bases 1 to 890) Loftus, B., Wang, Z., Van *l* Entamoeba histolytica RF Entamoeba histolytica Sheared genomic survey secuence histolytica GI:15302963 Aken, S. and Fraser, C. Entamoeba DNA Entamoeba histolytica

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Institute for Genomic Research 9712 Medical Center Dr., Rockville,
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The Institute
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Contact: Brendan J Loftus
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ATATTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGG
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/note="Vector: pHOS1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytic
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
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Email: huchanghua@263.net
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/note="obtained through DNA subtraction using the
nonpathogenic strain Leptospira biflexa serovar Pat
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Clones are derived from
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Department of Eukaryotic Genomics
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                                                                                                               TGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACCTCCATCTCCAGACGCAGATGT 1761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst_I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification.
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/strain="HM1:IMSS"
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196; Conserv
                                                                                                                                                                                                                                                                Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enqui humquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 150M6. part of the Daniokey BAC Library created by R. Plasterk and Keygene. Further details:
                                                                                                                                                                                                                                                                                                                           Submitted (13-MAR-2003) The Sanger Institute, Campus, Hinxton, Cambridgeshire, CB10 1SA, UK.
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 829)
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Danio rerio
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                                                                                                                         /tissue_type="Testis"
/note="vector pIndigoBAC-536"
103 c 32 g 434 t
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/clone="DKEY-150M6"
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Fax:
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1 (bases 1 to 843)

Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences
HM1: MSS sheared DNA library
                                                                                                                                                                                                                                                                                                        Email: bjloftus@tigr.org Clones are derived from
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                                                                                                                                                                                                                                                                                                                                                                        Department of Eukaryotic Genomics
The Institute for Genomic Research
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        /Clone lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site 1: Bst 1; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
 whole genome shotgun sequencing
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/strain="HM1:IMSS"
/db_xref="taxon:5759"
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Barell, Oxford University Press, 1999)
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Fax: 301 838 3543
Email: bilof.
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Contact: Brendan J Loftus
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Determination of clone end sequences from Entamoeba histolytica
HM1: MSS sheared DNA library
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/note="Vector: pHOS1; Site_1: Bst I; Constructed at
Institute for Genomic Research (TIGR), Rockville, MI
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Loftus,B., Van Aken,S. and Fraser,C.
Determination of clone end sequences
HM1:IMSS sheared DNA library
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Entamoeba histolytica
Eukaryota; Entamoebidae;
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Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute for Genomic Research 9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: M13-Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bjloftus@tigr.org
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Barell, Ox
a 34 c
                                     method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
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strain="HM1:IMSS"
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REFERENCE
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KEYWORDS
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville
                                                         Unpublished
Contact: Brendan J Loftus
                                                                                                   Eukaryota; Entamoebidae; Entamoeba.

(bases 1 to 849)

Loftus,B., Van Aken,S. and Fraser,C.
Determination of clone end sequences
HM1:IMSS sheared DNA library
                                                                                                                                                                                                                                                        AZ546009.1 GI:11167130 GSS.
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Medical Center Dr., Rockville,
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Pred. No. 0.0082;
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MD 20850, USA
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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
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Fax: 301 838 3543
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GGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCA 1789
                                                                                                                                                        ATAATCAGTGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATT
                                                                                                                                                                                                                GATGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAA
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/note="Vector: pHOS1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.) The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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'strain="HM1:IMSS"
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Pred. No. 0.016;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Loftus, B., Wang, Z., Van Aken, S. and F
Determination of clone end sequences
HM1:IMSS sheared DNA library (2001)
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ENTQV49TR Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: .Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entambeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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/strain="HM1:IMSS"
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Pred. No. 0.037;
0; Mismatches 363;
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Sheared DNA Entamoeba histolytica
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoggawa and Maron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
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Submitted (02-JUN-1999) Genoscope
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Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                            GSS.
Entamoeba histolytica
Entamoeba histolytica
                                                      Unpublished
                                                                     1 (bases 1 to 900)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences
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/mol_type="genomic DNA"
/db xref="taxon:7227"
/clone="BACR08K10"
/clone_lib="APCI-98"
/note="end : TET3"
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Fax: 301 838 3543
Email: bjloftus@tigr.
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/note="Vector: pHOS1; Site_1: Bst I; Constructed &
Institute for Genomic Research (TIGR), Rockville,
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AZ550256.1 GI:11175557
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1 (bases 1 to 905)
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                                       AATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGAT 1429
  TATGATAAAGCATATAATCTGTTAACTGAGGCTCATA-----AAGCCTTGTTTGNA 1369
                                                                                                                                                                   AGTGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Entamoeba histolytica Sheared DNA" /note="Vector: pHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR); Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytic using a method described by Clark and Diamond (Clark, C.G., and Diamond, I.S. (1993) Entamoeba histolytica: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HM1:IMSS"
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Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
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Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 645)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: carlton@tigr.org
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                                                                                                            /note="Vector: pAD-GAL4; At 20-25% parasitemia, blood collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method,
                                                         mRNA isolated using oligo(dT)-cellulose chromatography First strand cDNA synthesis was completed using a 50-ba primer and reverse transcriptase in the presence of
                     5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI
adaptors ligated to the blunt ends.
                                                                                                                                                                                                                       /dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/clone_lib="PyBS"
                                                                                                                                                                                                                                                                                                                                                 mol_type="mRNA"
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Plasmodium yoelii yoelii cDNA clone PYCML60
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                                                                                                                                                                                                                                                                                   Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 747)
Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W.,
Fraser, C.M. and Carucci, D.J.
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EST565255 PyBS Plasmodium yoelii
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                                                                                                                                                                                             Reagent Resource Center,
                                                                                                                                                                                                           For clone info, please contact the
                                                                                                                                                                                                                                                   Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                      Contact: Jane Carlton
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                /db_xref="taxon:73239"
/clone="PYCKW24"
                                                        /strain="17XL"
                                                                                        /organism="Plasmodium
                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.48;
_stage="Asexual blood stages"
                                                                          type="mRNA"
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Pred. No. 0.12;
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                                                                                            yoelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA linear EST 04-DEC-2001 yoelii cDNA clone PYCKW24 5' end,
                                                                                                                                                                                                             Malaria Research
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                                                                                            yoelii"
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REFERENCE
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SOURCE
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VERSION
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AZ535744/c
                                                                                                               COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 170;
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Best Local Similarity
                                                                                                                                                                              TITLE
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                                                                                                                                                                                                                                           Entamoeba histolytica
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
                                                                                                                                                                                                                                                                                                                                                                                                     AZ535744 816 bp DNA linear GSS 03-NOV-2000 ENTCQ25TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
9712 Medical Center Dr., Rockville, Tel: 301 838 0208
Fax: 301 838 3543
                                                            Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                     1 (bases 1 to 816)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences
HM1:IMSS sheared DNA library
                                                                                                                                                                                                                                                                                                                                                             genomic, genomic AZ535744
                                                                                                                                                                                                                                                                                                                                        AZ535744.1
                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGATGAAGATGAAGAAGATGACGATGATTCTAAAAAAGAAGATGGATCAAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACGATGACGATGACGATGATGAAGACGATGATGAGGATGAAGATGATGAAGATGAT 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACGATGATGATGACGACGATGAAGATTTTGAAGATATGGATGATGATGATGATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGATGATGACGACGATGAAGATGACGATGAAGACGATGATGATGAAGACGACGATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5-methyl GCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and ECORI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using ECORI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="PyBS"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blc
collected from BALB/cByJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose collumns. Total RNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated."
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                                                                                                                                                                                                                                                                                                                                        GI:11092691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56.6; DB Pred. No. 0.13;
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                                            20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              746 AAGACGATGATGAAGATGATGAAGAAGAAGATGATGAAGATGACGATGATGATGAAG
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High quality sequence start: 36
High quality sequence stop: 816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA library
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GCTATACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAAC
                                                                                                  ACGATGATGAAGAAGACGATGATGAAGAAGACGATGAAGAAGAAGACGATGAAGAAGAAG
                                                                                                                                                                                  ATCATTACCATAATATTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATG
                                                                                                                                                                                                                                                                            ACGATGATGAAGAAGACGATGATGAAGAAGACGATGATGAAGAAGACGATGATGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                CATATATGGTTGAGCATACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGATGAAGAAGACGATGAAGAAGACGATGAAGAAGACGATGAAGAAGACGATGAAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCGTATTGCTCAATTAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAAC 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTACCCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bjloftus@tigr.org
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/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="HM1:IMSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:5759"
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RESULT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For clone info, please contact the Malaria Research Reagent Resource Center, ATCC http://www.malaria.mr4.org/mr4pages/index.html
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The Institute for Genomic Research
9712 Medical Center Drive, Rockvil
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Plasmodium yoelii yoelii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Jane Carlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                       273
                                                                                                                             with XhoI and separated on a Sephacryl S-500 column. Size-Fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                      isolated using the guanidinium isothiocyanate method, and mRNA isolated using Oligo(GT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and ECORI adaptors ligated to the blunt ends. The sample was cleaved
                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="PyBS"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blc
collected from BALB/cByJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose collumns. Total RNA was
                                                                                                           isolated."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:73239"
/clone="PYCLB13"
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lab_host="E. coli XL-1 Blue"
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RESULT 18
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
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EST562775 PyBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Jane Carlton
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Fraser, C.M. and Carucci, D.J.
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parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guandidnium isothiocyanate method, and mRNA isolated using oligo(dT) cellulose chromatography. First strand cDNA synthesis was completed using a 50-bai primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis uneven
                                                                                                   /clone lib="PyBS"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blocollected from BALB/cByJ mice infected with Py17XL
                                                                                                                                                                                                                              /organism="Plasmodium yoelii yoelii"
/mol_type="mRNA"
                                                                                                                                                  /dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
                                                                                                                                                                                 /db_xref="taxon:73239"
/clone="PYCJO90"
                                                                                                                                                                                                              strain="17XL"
                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                             . 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:17305933
                                                                                                                                                                                                                            _type="mRNA"
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PYCJO90 5' end,
                                                                                                                                                                                                                                                                                                                                     and
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Query Match
Best Local Similarity
GAGGATGAAGATGAAGAAGATGACGATGATTCTAAAAAAGAAGGTGGATCAAATGC
                                                                                          GACGATGACGATGACGATGAGGACGATGAGGATGAGGATGAGGATGAAGATGAT
                                                                                                                                                                                                                                                                                  GAAGATGACGATGATGAAGATGATGATGATGACGACGACGATGATGATGGAGATGAT
                                                                                                                                                                                                                                                                                                                                                                          GÁCGATGATGACGATGACGATGACGATGACGATGATGATGATGATGATGATGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATGAGGTTAGCAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGAC 166
                                            AAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGC
                                                                                                                                      GACGATGATGATGACGACGACGATGAAGATTTTGAAGATATGGATGATGATGATGAT
                                                                                                                                                                                                                                    GATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTT
                                                                                                                                                                                                                                                                                                                                 GACGCTATCATCAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGATGATGACGACGATGAAGATGACGATGAAGACGATGATGAAGACGACGATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adaptors ligated to the blunt ends. The sample was cleawith KhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-KhoI cleaved at After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                termini were treated with Pfu DNA polymerase and EcoRI
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Pred. No.
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Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockvil
                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
                                                                                                                                               For clone info, please contact the Malaria Research and Reagent Resource Center, ATCC
                                                                                                                                                                                                                                                                                                                                Fraser, C.M. and Carucci, D.J. Plasmodium yoelii EST project at
                                                                                                                                                                                                                                                                                                                                                                       Carlton, J.M., Daly, T.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM168242
                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Alveolata; Apicomplexa; Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM168242.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
                                                                                                                           http://www.malaria.mr4.org/mr4pages/index.html
                                                                                                                                                                               Email: carlton@tigr.org
                                                                                                                                                                                                     Fax: 301-838-0208
                                                                                                                                                                                                                        Tel: 301-530-9319
                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to
                                                                                                            primer:
               /mol_type="mRNA"
/strain="17XL"
                                                    /organism="Plasmodium
                                                                                          Location/Qualifiers
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                                                                           . 694
                                                                                                              AUT
_xref="taxon:73239"
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n yoelii yoelii
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                                                                                                                                                                                                                                                                                                                                                                     Vaidya, A.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 04-DEC-2001
PYCOX60 5' end,
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VERSION
KEYWORDS
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BM160500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 CAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTAT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 GATGAGGTTAGCAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGAC 166
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockvil
                                                                                                              Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 717)
Carlton,J.M., Daly.T.M., Long,C.A., Bergman,L.W., Vaidya,A.B
Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
                                                                                                                                                                                                                                                                                                                                                                    BM160500 717 bp mRNA linear EST563023 PyBS Plasmodium yoelii yoelii cDNA clone
                                                                     Contact: Jane Carlton
                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                        BM160500.1 GI:17306181
                                                                                                                                                                                                                                                                                                                                BM160500
                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="PyBS"
/clone lib="PyBS"
/clone lib="PyBS"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over parasites, and leukocytes removed by passage over parasites, and leukocytes collumns. Total RNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and
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lab_host="E. coli XL-1 Blue"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187
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  Rockville,
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0.28;
    MD 20850,
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    USA
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PYCJS13 5' end,
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Best Local S
Matches 169
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В Ś 멍 Ş В δ 밁 ş 망

COMMENT

TITLE

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167 CAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTAT 226
                                                                                                                                                                                                                                                                            505 GAGGATGAAGATGAAGAAGATGACGATGATTCTAAAAAAAGAAGGTGGATCAAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 GÁCGATGATGACGATGACGATGACGACGATGATGATGATGATGATGACGATGATGAA
                            mRNA sequence.
BM162492
                                                                                         BM162492 756 bp mRNA linear EST 04-
EST565015 PyBS Plasmodium yoelii yoelii cDNA clone PYCKT28
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For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
BM162492.1 GI:17308173
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Tel: 301-530-9319
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Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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The Institute for Genomic Research
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                                     GACGATGATGATGACGACGATGAAGATTTTGAAGATATGGATGATGATGATGAT
                                                                                                                      GATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTT
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/note="Vector: pAD-GAL4; At 20-25% parasitemia, blocollected from BALB/cByJ mice infected with Py17XL
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Fraser,C.M. and Carucci,D.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parasite Genomics Group
The Institute for Genomic
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                                                                  GATGATGATGACGACGATGAAGATGACGATGAAGACGATGATGAAGACGACGATGAC
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                                                                                                       GATGAGGTTAGCAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGAC
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                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                              /Clone lib="PyBS"
//Clone lib="PyBS"
//Clone lib="PyBS"
//note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was //note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhOI and separated on a Sephacryl S-500 column.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carlton@tigr.org
                                                                                                                                                                                                                                                       isolated."
60 c
                                                                                                                                                                                                                                                                                              Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Plasmodium
/mol_type="mRNA"
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'lab_host="E. coli XL-1 Blue'
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TITLE
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Entamoeba histolytica
Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: bjloftus@tigr.org
Clones are derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                              /clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
the common shortune convencion.
                                                                                   whole genome shotgun sequencing projects. In Gen
Sequencing: A Practical Approach, eds. M. Vaudin
Barell, Oxford University Press, 199)."
72 c 175 g 229 t
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HM1:IMSS"
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                                                                                                                                                                                                                                                                                                                                                                                                                 _xref="taxon:5759"
2.3%;
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                             Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 823)

Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences
HM1:IMSS sheared DNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                                                                                                                                                                            Class: shotgun
                                                                                                                                                                                                                                                                              Seq primer: M13-Reverse
                                                                                                                                                                                                                                                                                               DNA library
                                                                                                                                                                                                                                                                                                                               Email: bjloftus@tigr.org
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            Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
                                                                 /clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at
/notitute for Genomic Research (TIGR), Rockville, M
method for isolate identification.
                                                                                                                                    /organism="Entamoeba histolytica"
/mol_type="genomic_DNA"
/strain="HM1:IMSS"
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Entamoeba histolytica Sheared
                                                                                                                  db_xref="taxon:5759"
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RESULT 25
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               High
High
                                                                                                                                                                                                                                                                                                                         genomic, genomic survey sequence.
BH139532
BH139532.1 GI:15098593
GSS.
                                                                                                 Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
                                                                                                                                         The Institute for Genomic 9712 Medical Center Dr.,
                                                                                                                                                             Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                    Loftus, B., Wang, Z., Van Aken, S. and Fraser, C. Determination of clone end sequences from Ent HMI: MSS sheared DNA library (2001)
                                                                                                                                                                                                                                                                                                                                                                                  BH139532 843 bp DNA linear GS ENTNG88TF Entamoeba histolytica Sheared DNA Entamoeba
                                          Seq primer: M13-Forward
Class: shotgun
                                                                                                                                                                                          Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                            Entamoeba histolytica
Entamoeba histolytica
                                                                         DNA library
                                                                                       Clones are derived from the
                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                 Eukaryota; Entamoebidae; Entamoeba
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quality sequence start: 4 quality sequence stop: 714 Location/Qualifiers
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Rockville,
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RESULT 26
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/note="Vector: pHOS1; Site_l: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification.
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/strain="HM1:IMSS"
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DEFINITION
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Nori Satoh unpublished cDNA library, gastrula and neurula
ACCESSION
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VERSION
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VERSION
BW141179.1 GI:24498404
KEYWORDS
SOURCE
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.

REFERENCE
JOURNAL
TITLE
JOURNAL
COMMENT
CONTACT: Nori Satoh
Department of Zoology

MIATION CONTACT: NORI SATOH
DEPARTMENT

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                                                                                                                                                                          bw144040 Nori Satoh unpublished cDNA library, gastrula and r. Ciona intestinalis cDNA clone rcign067b16 3', mRNA sequence. BW144040
Eukaryota; Metazoa; Chordata; Urochordata; Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 656)
Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
                                                                                        Ciona intestinalis
Ciona intestinalis
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                           BW144040.1 GI:24501265
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/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcign058f11"
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/dev_stage="gastrula and neurula"
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Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 844)
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                                                                                                                               Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kyoto University
Sakyo-ku, Kyoto, Kyoto
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/db_xref="taxon:7719"
/clone="rcign067b16"
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/clone_lib="Nori Satoh unpublished cDNA library,
and neurula" 66 g 260 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue_type="whole body"
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Huckle, E.
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Pred. No. 0.55;
D; Mismatches 244;
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and Durham, J.L.
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REFERENCE
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CD099026
                       JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Campus, Hinxton, Cambridgeshire, CB10 1SA, UK.
humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of
part of the Daniokey BAC Library created by R.
Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
                                                                                                                                                                               AGENCOURT 14011375 NICHD XGC Tad1 IMAGE:6939285 5', mRNA sequence.
           Contact: Robert Strausberg, Email: cgapbs-r@mail.nih.go
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                  Unpublished
                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                               Xenopus laevis
                                                                                                                                                                  CD099026.1 GI:30752129
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                                                                                            Kenopodinae; Kenopus.
                                                                                                                                          Kenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                                                                                                         GCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATACTGGTG
                                                                                                                                                                                                                                                                                                                                                                                             ATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCAAGGAC
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                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 752)
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                                               Gene Index
  Procurement: Drs.
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/note="vector pIndigoBAC-536"
49 c 81 g 308 t
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/db_xref="taxon:7955"
/clone="DKEY-99E7"
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Pred. No. 0
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and Liquan Cai
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K. E-mail e
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                                                        Project
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Best Local
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Satou, Y., Shin-i, T., Kohara, Y. and Satoh, Expressed genes in Ciona intestinalis (20 Unpublished
                                                                                                                                                                                                                                                                           BW273704 Nori Satoh unpublished cDNA library, gastrula and neurula Ciona intestinalis cDNA clone cign067b16 5', mRNA sequence.
                                                                                                    Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia; Cionidae; Ciona.
                                                                                                                                                       Ciona intestinalis
                                                                                                                                                                                                                                 BW273704.1
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                                                                                                                                                                                 Ciona intestinalis
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution info
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACCATGATGATGACCAACAAC 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAACAAGAGCATAGTCAACATC 428
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                                                                            (bases 1 to 671)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /notce="Organ: Developing Tadpole; Vector: pDNR-LIB;
/notce="Organ: Developing Tadpole; Vector: pDNR-LIB;
Site 1: Sfi; Site 2: Sfi; 5' and 3' adaptors were used i:
cloning as follows: 5' adaptor sequence:
5'-CACGGCCATTATGCCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGGCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.6
(range 0.9-3.0 kb). 15/15 colonies contained inserts by
PCR. This library was enriched for full-length clones an
was constructed by Clontech Laboratories (Palo Alto, CA)
a 128 c 208 g 169 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="metamorphosis stage
/clone_lib="NICHD_XGC_Tad1"
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'db_xref="taxon:8355"
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                                                                                                                                                                               AZ530768 890 bp DNA linear GS ENTBH54TF Entamoeba histolytica Sheared DNA Entamoeba genomic, genomic survey sequence.
AZ530768
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.
               1 (bases 1 to 890)
Loftus, B., van Aken, S. and Fraser, C.
Determination of Clone end sequences
HM1:IMSS sheared DNA library
                                                                                                      Entamoeba histolytica
Entamoeba histolytica
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                                                                                       Eukaryota; Entamoebidae;
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67 c
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/mol_type="mRNA"
/db_xref="taxon:7719"
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/tissue_type="whole body"
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clone_lib="Nori Satoh unpublished cDNA library,
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Fax: 301 838 3543
Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 20 High quality sequence stop: 822
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/note="Vector: pHOS1; Site 1: BSt I; Constructed at The
/note="Vector: pHOS1; Site 1: BSt I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.) The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="HM1:IMSS"
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                                                                                                                                                                                                                                                           Matches 146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
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  370
                                           284
                                                                                   310
                                                                                                                          224 TATGACGCTATCATCAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGAT
                                                                                                                                                                          250
                                                                                                                                                                                                                164 GACCAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 677)
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Plasmodium yoelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: ADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carlton, J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM161314.1 GI:17306995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: carlton@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium yoelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser, C.M. and Carucci, D.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM161314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.malaria.mr4.org/mr4pages/index.html
                                      GAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTAT 343
                                                                                                                                                                       GACGACGATGATGACGATGACGATGACGACGATGATGATGATGATGATGACGATGAT
GATGACGATGATGATGACGACGATGAAGATTTTTGAAGATATGGATGATGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                        288
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EccRI-XhoI cleaved at After packaging, the phagemid vector (pAD-CAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Tector: pAD-GAL4; At 20-25% parasitemia, blc collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was microcrystalline cellulose collumns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolated using the guanidinium isothiocyanate method,
                                                                                                                                                                                                                                                                                                                                                                                            isolated."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strain="17XL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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                                                                                                                                                                                                                                                                             2.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _xref="taxon:73239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B.,
                                                                                                                                                                                                                                                                                                                                                                        50 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lib="PyBS"
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                                                                                                                                                                                                                                                                                                                                                                   186 g
                                                                                                                                                                                                                                                                                Score 52.4;
Pred. No. 1;
                                                                                                                                                                                                                                                           Mismatches 156;
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BASE COUNT
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AUTHORS
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BM169486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              550 GC 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   404 CAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B., Fraser,C.M. and Carucci,D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For clone info, please contact the Malaria Research and Reference Reagent Resource Center, ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parasite Genomics Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Jane Carlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium yoelii EST project at TIGR
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BM169486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: ADF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: carlton@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301-530-9319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BM169486.1 GI:17302718
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                           263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      //www.malaria.mr4.org/mr4pages/index.html
                                                                       primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                            /dev_stage="Asexual blood stages"
/lab_host="B. coli XL-1 Blue"
/clone_lib="PyBS"
/clone_lib="PyBS"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
                                                       isolated."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="17XL"
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                      156 g
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Query Match 2.2%; Best Local Similarity 48.3%; Matches 146; Conservative

Score 52.4; DI Pred. No. 1; 0; Mismatches

DB 12; 156;

Length Indels

725; 0,

Gaps

0

41

and B.

0;

Gaps

2123 76

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281 GATGAGGATGAAGATGAAGAAGATGACGATGATTCTAAAAAAGAAGGTGGATCAAAT 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             866 bp DNA linear GSS 03-NOV-2000 ENTCA79TR Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Entamoeba histolytica
Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13-Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: bjloftus@tigr.org
Clones are derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Loftus,B., Van Aken,S. and Fraser,C. Determination of clone end sequences HM1:IMSS sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Entamoebidae; Entamoeba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ527885.1 GI:11080056
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                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence start: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 838 3543
               /clone_lib="Bntamoeba histolytica Sheared DNA"
/note="Wector: pHOS1; Site_1: Bst 1; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.) The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
                                                                                                                                                                                                                                                                                                                    /organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HM1:IMSS"
                                                                                                                                                                                                                                                                                             db_xref="taxon:5759"
                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
genome shotgun sequencing
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projects.
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High quality sequence start: 38
High quality sequence stop: 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Loftus,B., Wang,Z., Van Aken,S. and Fraser, Determination of clone end sequences from E HM1:IMSS sheared DNA library (2001)
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Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Entamoebidae; Entamoeba (bases 1 to 976)
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               /clone lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site 1: Bst 1; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G. and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing: A Practical Approach, eds. M. Vaudin
Barell, Oxford University Press, 1999)."
116 c 181 g 216 t
                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="HM1:IMSS"
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histolytica

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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries: A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                        Submitted (02-JUN-1999) Genoscope - BP 191 91006 EVRY cedex - FRANCE (E-
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster
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Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                                                                              Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockvil
                                                                                                                                                                                                                                                                                                                                         Carlton, J.M., Daly, T.M., Long, Fraser, C.M. and Carucci, D.J. Plasmodium yoelii EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
                                                                                                                                                    For clone info, please contact the Malaria Research and Reference Reagent Resource Center, ATCC
                                                                                                                                                                                                            Tel: 301-530-9319
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                      Contact: Jane Carlton
                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                  http://www.malaria.mr4.org/mr4pages/index.html
                                                                                                                                                                                        Email: carlton@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
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                                                                                                                   primer: ADF
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   /mol_type="mRNA"
/strain="17XL"
/db_xref="taxon:73239"
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/note="end : TET3"
149 c 155 g
                                                           /organism="Plasmodium
                                                                                                Location/Qualifiers
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/db_xref="taxon:7227"
/clone="BACR16N06"
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Pred. No. 1.3;
6; Mismatches 155;
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yoelii yoelii
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EST 04-DEC-2001 PYCPV42 5' end,

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REFERENCE
AUTHORS
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KEYWORDS
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AZ529191/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
                                                    Tel:
                                                                 Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                             Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 880)
                                                                                                                                                                                                                                                                                                                                        AZ529191 880 bp DNA linear GSS 03-NOV-20 ENTBV68TR Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.
                                 Fax:
                                                                                                                                                                                                                                                                                                                         genomic, genomic
AZ529191
                                                                                                                       Contact: Brendan J Loftus
                                                                                                                                          Unpublished
                                                                                                                                                            HM1:IMSS
                                                                                                                                                                           Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences
                                                                                                                                                                                                                                                                   Entamoeba histolytica
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301 838 3543
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           bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pAD-GAL4; At 20-25% parasitemia, blood collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was
                                                                                                                                                          sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base rist strand cDNA synthesis was completed using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer and reverse transcriptase in the presence of
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/lab_host="E. coli XL-1 Blue"
/clone_lib="PyBS"
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derived from the Entamoeba histolytica HM1: IMSS sheared
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Pred. No. 1.2;
0; Mismatches 137;
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331 AGÁCGAAGATGATGAAGACGAÁGATGATGAAGACGAAGATGATGAAGACGAAGATGATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257; · Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence start:
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Class: shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGCTGC 363
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                                                              AGCTAGCGAGTTGGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAATT
                                                                                                                                                                             TGATGCTTATATCGTTCCTCATGAGAATCATTACCATTACATTCCTAAGAATGAGTTATC 603
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AGACGAAGATGATGAAGACGAAGATGATGAAGACGAAGATGATGAAGACGAAGATGATGA 212
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                                                                                                                             TGATGATGAAGACGAAGATGATGAAGACGAAGATGATGATGATGTAGTCCCATACGTATC 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."

271 c 67 g 413 t
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mol_type="genomic DNA"
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RESULT 39
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AL179594.1 GI:7817651
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Teleostei; Euteleostei; Neoteleostei;
Actinopterygii; Neopterygii; Percomorpha; Tetraodontiformes;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Teradontoidea; Tetraodontidae; Tetraodon.
                        366
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                                                              261
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                                                                                                                                                                                                                                                        186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-APR-2000) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr) - Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a lauscale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of freshwater pufferfish Tetracdon nigroviridis

Genome Res. 10 (7), 939-949 (2000)
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roest Crollius, H., Jaillon, O., Dasilva, C., Bound Bernot, A., Fizames, C., Wincker, P., Brottier, P., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                            Similarity
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ACGCGGATAACGTCCGTACAAAAGAGGGAAATCAATCGACAAAAACAAGAGGCATAGTCAAC
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                                                            AGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGCTGCCC
                                                                                                                                      AAGATWTCAATAATGATGGTGATGGTTATGAAGATWATAATGATAATGATGAAGATWTCA
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PUC-Ori"
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|mol_type="genomic DNA"
|db_xref="taxon:99883"
|clone="233A11"
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AU088119 Sugano N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: jwatanab@manage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagdwa,K., Maruyama,K., Suyama,A. and Sug
S. Construction and characterization of a full length-enriched
a 5'-end-enriched_DNA_library Gene 200 (1-2), 149-156 (1997).
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The University of Tokyo, Department of Parasitology
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Plasmodium
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EST.
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1 (bases 1 to 500)
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/clone_lib="Sugano Malaria cDNA
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/clone="XPFn6549"
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/mol_type="mRNA"
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Seq primer: SP6
Class: BAC ends
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AZ196050 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 78650 
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Strongylocentrotus purpuratus
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Echinoida,
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California Institute of Technology
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Location/Qualifiers
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(626) 793-3047
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urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db xref="taxon:7668"
/clone="Plate=1031 Col=10 Row=I"
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AL419462.1
GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: segref@genoscope.cns.fr) Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, saccharomyces servazzii, Elyoscomyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    de Montigny,J., Spehner,C., Souciet,J.,
Wincker,P., Artiguenave,F. and Potier,S
Genomic exploration of the hemiascomycet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pichia farinosa
Pichia farinosa
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T3 end of clone AX0AA039F08 cof Pichia farinosa, genomic s
                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 kb were prepared and both extremities were sequenced. keywords for description of this sequence and for the set the other extremity of this insert.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                  ACCACAAGAAAAGAAAGTCCTGGTTGATGCTGTTGATAAAATTAAAGMAAAAWGGWAA 88
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM167469
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The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: carlton@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium yoelii EST project at TIGR
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Fraser,C.M. and Carucci,D.J.
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                                                                                                                                                                                                     /Clone="FICORS"
//dev_stage="Abexual blood stages"
//dev_stage="Abexual blood stages"
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adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipited and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jane Carlton
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yoelii yoelii cDNA clone PYCOK56 5' end,
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                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang,K., Cole,R., Chakrabarti,D., Haywood,R., Clifton,S., Pape,D., Marra,M., Hillier,L., Martin,J., Wylle,T., Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,E., Ronko,I., Tsagareishvili,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A., Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D., Waterston,R., Wilson,R. and Sibley,D.
                                                                                                                                                                                  Email: est@watson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA
Washington University Genome Sequencing Center For
obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Seq primer: -40UP from Gibco
High quality sequence stop: 421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BU496963 555 bp mRNA linear PfESToab61c09.yl Plasmodium falciparum 3D7 asexual falciparum 3D7 cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: L. David Sibley
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1 (bases 1 to 555)
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Location/Qualifiers
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/mol type="mRNA"
/db xref="taxon:36329"
/lab host="DH10B (GeneHog, Invitrogen, Inc.)"
/clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
/clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
/note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
                                                                                                                       organism="Plasmodium falciparum"
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                                                                                                                                                 Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 707)
Carlton,J.M., Daly.T.M., Long,C.A., Bergman,L.W., Vaidya,A.B
Fraser,C.M. and Carucci.D.J.
Plasmodium yoelii EST project at TIGR
                                              Parasite Genomics Group
The Institute for Genomic Research
                                                                                                  Contact: Jane Carlton
                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                       BM164483.1 GI:17310164
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Medical Center Drive, Rockville, 301-530-9319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total RNA samples were isolated from mixed stage saponin(0.1%)-lysed P. falciparum 3D7 infected erythrocytes by the acidic guanidinium-phenol chloroform method. The poly A+ RNA was isolated by the polyAT-Tract mRNA isolation system (Promega, WI) using streptavidin Magnesphere particles. Directional CDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EcoRI and XhoI sites of 1 ZapII vector using the Zap CDNA inserts in the library was between 1.0 and 1.5kb. Clones were mass excised using the ExAssist helper phage (Stratagene), the phagemids were preciptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells."
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yoelii yoelii cDNA clone
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2288 CTTCAAATTATGGATAACAATAGTATCATGGCAGAAAGGCAGAAAAATTACTTGCGTTGTTA 2347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1808 GTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCATACAGTT 1867
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                                                                                                                                                                                                                                                     GACGATGAAAAAGAAGATGAACTAGACGATGAAAAAGAAGAAGATGAAAAAGAAGAAGATGAACTA 344
                                                                                                             GATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAATTTGACT 228:
                                                                                                                                                            GACGATGAAAAAGAAGATGAACTAGACGATGAAAAAGAAGATGAACTAGACGATGAAAAA 284
                                                                                                                                                                                                      GCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGGAAGATTTGTTT 1987
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                                                                                                                                                                                                                                                                                             TTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTA 2167
                                                                                                                                                                                                                                                                                                                                                GAAGATGAACTAGACGATGAAAAAGAAGATGAACTAGACGATGAAAAAAGAAGATGAAAAAA 404
                                                                                                                                                                                                                                                                                                                                                                                      GGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCACAGTGAAGATCCAAATAAGAAC 2107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=Tvector: pAD-GAL4; At 20-25% parasitemia, blood collected from BAIB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, isolated using the guanidinium isothiocyanate method.
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/lab_host="E. coli XL-1 Blue"
/clone_lib="PyBS"
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/strain="17XL"
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167 CAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTAT 226
                                                                                     107 GATGAGGTTAGCAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGAC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reagent Resource Center, ATCC http://www.malaria.mr4.org/mr4pages/index.html Seq primer: ADF.
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Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
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BM170666.1 GI:17303898
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Fax: 301-838-0208
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For clone info, please contact the Malaria Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: carlton@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium yoelii yoelii
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                                                                                                                                                                                                                                            isolated."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with PylTXL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanddinium isothiocyanate method, and
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/lab_host="E. coli XL-1 Blue"
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Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parasite Genomics Group
The Institute for Genomic |
9712 Medical Center Drive,
Tel: 301-530-9319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished Contact: Ja
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: carlton@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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//dev_stage="%asexual blood stages"
//lab_host="E. coli XL-1 Blue"
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strain="17XL"
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BJ073162 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL109b17 5', mRNA sequence.
                                                                                                                                                                                                                                                               Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                             Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                      Expressed genes in X. laevis embryo
                                                                                                                                                                                                                                                                                                                                                                   Kitayama, A.,
                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog)
Xenopus laevis
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ilarity 46.7%;
Conservative
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Location/Qualifiers
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/db_xref="taxon:8355"
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clone_lib="NIBB Mochii normalized
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                                                                                                                                  clone="XL109b17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.malaria.mr4.org/mr4pages/index.html
Seq primer: ADF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parasite Genomics Group
The Institute for Genomic
9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
Contact: Jane Carlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 687)
Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W.,
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: carlton@tigr.org
For clone info, please contact the Malaria Research
Reagent Resource Center, ATCC
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                                                                                                    /note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo (dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of
5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EccRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to
                                                                                                                                                                                                                                                /dev_stage="Asexual blood stages"
/lab_host="E_coli XL-1 Blue"
/clone_lbe="PyBS"
/note="Vector: pAD-GAL4; At 20-25;
                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:73239"
clone="PYCPU72"
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                                                                                                                                                               http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOCAP005AF01NP1&cluster=5744.r.
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation
Faraday Avenue Genoscope sequence ID : CSOCAP005AF01NP1.
                                                                                                                                                                                                                                                  Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5744.r
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                    Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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1 (bases 1 to 1044)
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/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was
                                                          clone="CS0CAP005YK01"
                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Sequence 187, App Sequence 185, App Sequence 215, App Sequence 217, App Sequence 266, Appli Sequence 327, App Sequence 327, App Sequence 1027, App Sequence 1027, App Sequence 1191, Appli Sequence 1191, Appli Sequence 11, Appli Sequence 11, Appli Sequence 1, Appli Sequence 203, Appli Sequence 1, Appli Sequence 207, Appli Sequence 1, Appli Sequence 1, Appli Sequence 5, Appli Sequence 207, Ap
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US-08-961-083-55
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: P340P2
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 2389 base pairs
TYPE: nucleic acid
GTBANDENNESS:
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 2389; Conserv
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MEDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICANT: Choi e
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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COUNTRY:
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CITY: Rockville
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9410 Key West Avenue
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                                                         TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320
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                                                                            TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG
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RESULT 2
US-09-536-784-55
           Sequence 55, Application US/09536784
Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptoco
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APPLICATION NUMBER: 08/961,083

APPLICATION NUMBER: 08/961,083

FILING DATE: OCT-30-1997

ATTORNEY/AGENT INFORMATION:

NAME: MICHAELE S. MARKS

REGISTRATION NUMBER: 41,971

REFERENCE/DOCKET NUMBER: PB340P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEPHONE: (301) 309-8512

INFORMATION POR SEO ID NO: 55:

SEQUENCE CHARACTERISTICS:
LENGTH: 2389 base pairs

TYPE: nucleic acid

corpandeducts: double
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/536,784
FILING DATE: 30-0ct-1997
CLASSIFICATION: CUNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: double TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS;
CORRESPONDENCE ADDRESSES
ADDRESSES Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
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               AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC
                                                                     TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA
                                                                                                                                             GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTTACCTTAAGGATGC
                                                                                                                      GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC
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                                             TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA
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; NUMBER OF SEQ ID NOS: 14 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 9		nd B Having Selected St	Comprising Str	RESULT 3 US-09-468-656A-9 ISequence 9, Application US/09468656A . Datent NO 658706	TAAGTAAGGAAAAATAAAC	2281	221 AGIANCUSATICIAN INCANTROCANTROCANA ICANOCIO CANCIONA IA CONTROCANA IL CANCIONA IL CANC	2101 ICANGIAGNACISHAMANGIAGNACCCARCICANAGAGCAGCAGCTTTTGCTGCGAA	2101 TANGANCTI CANNOGRATIGA GAGAGGAGAGAGAGAGAGAGAGAGAGAGGAGAGAGA	2041	1991 IIIGIIIGGACGAITAAGIACIAGUAGAACACCCTGACGAACGICCACAIIGIAGIAGAACACCCTGACGAACGICCACAIIGIAGIAGIAGIAGIAGIAGIAGAACACCCTGACGAACGICCACAIITCTAATGA 1981 TITGITTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGICCACATTCTAATGA	1921 TARAFITTOCTTIGGTTTGATGATCACACACACAAAGCTCCAAATGCTATACCTTGGAAGA 1921 TARAFITTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTTGGAAGA 1921 TARAFITTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTTGGAAGA 1921 TARAFITTGCTTGGTTTGATGATCACCACATACAAAGCTTCCAAATGGCTATACCTTGGAAGA 1921 TARAFITTGCTTGGTTTGATGATCACCTTACAAAGCTTCCAAATGGCTATACCTTAATGA	1861 TACAGITGAGGITAAAAACGGIAATITGATIATICCTCAIAAGGATCAITACCAIAATAT	1801 CAATCGTGTAAAGGGAAAAACGAATTCCACTGTTCGACTTCCATATATGGTTGAGCA 1801 CAATCGTGTAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA	1/41 TCCATCTCCAGACGCAAATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTA 1/11	1741 TCCATTCTCAGAGGGAAAAGTTGCTAAAGGAAAGGTAAAGGAAAAGGTAATCTTA	1621 TGAAGGABABAACTTTGCAGCTCABGCCTATACTABAGABABAAGGTATCCTACC	Db 1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1620

	QY 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900	Qy 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840	OY 721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780	Qy 661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAACTGGGTACCTTC 720	OY 601 ATCAGCTAGCGAGTTGGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660	QY -541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600	-Qy 481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540	QY 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480 .	QY 361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC	OY 301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360	QY 241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300	OY 181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240	QY 121 GCGTGAAGGAATGCTGAGCAAATCGTCATGAAGATAACAGACCAAGGCTATGTCAC 180	QY 61 TATAGATGGAAACAAGCGAAGCGAAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120	QY 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60	Query Match 100.0%; Score 2388; DB 4; Length 2451; Best Local Similarity 100.0%; Pred. No. 0; Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	; NAME/KEY: misc feature ; LOCATION: (1). 7(2451) ; OTHER INFORMATION: n = a, c, t or g US-09-468-656A-9	
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Query Match 100.0%; Score 2388; DB 4; Length 8195; Best Local Similarity 100.0%; Pred. No. 0; Matches 2388; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	nucleic acid DNESS: doub Y: linear	TELEFAX: (301) 309-8512 ; INFORMATION FOR SEO ID NO: 94: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 8195 base pairs		APPLICATION NUMBER: ; FILING DATE: ; ATTORNEY/AGENT INFORMATION: ; NAME: BYOOKES, A. Anders		COMPUTER: HP VECTOR 486/33 COMPUTER: HP VECTOR 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CHERRY APPLICATION DATA.	COUNTRY: USA ZIP: 20850 COMPUTER READABLE FORM: MEDITUM TYPE: District 2 50 inch 1 Amh			US-08-961-527-94 US-08-961-527-94 ; Sequence 94, Application US/08961527 ; Patent No. 6420135 . GENERAL, INCOMMATION:	Db 2400 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAAATAAAC 2448	Db 2340 TTTGÁCTCTTCÁAATTATGGÁTÁACÁATÁGTÁTCÁTGGCÁGÁÁÁGÁÁÁÁÁTTÁCTTGC 2399 Qy 2341 GTTGTTAAAAGGAAGCATCTTGTAAGTAAGGAAAAATAAAT	QY 2281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGACAGAAAAATTACTTGC 2340	2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA	QY 2161 TCAAGTAGAGACTGAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGC	2101 TAAGAACTT CAAAGCGGATGAAGAGCCAGTAGAGAACACCTGCTGAGGCAGAAGTCCC	2100 TGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGA	Db 2040 TTTGTTTTGCGACGATTAAGTACTACGTTAGAACACCCTGACGAACGTCCACACATTCTAATGA 2099
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APPLICANT: Johnson, Leslie S.
APPLICANT: Adamou, John E.
TITLE OF INVENTION: Vaccine Compositions Comp:
TITLE OF INVENTION: Pneumoniae Group A and B
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-444
CURRENT APPLICATION NUMBER: US/09/468,656A
CURRENT FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 11
SEQ ID NO 11
LENGTH: 2531
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
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Vaccine Compositions Comprising Streptococcus
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Pred. No. 8.9e-263;
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RESULT 6 US-09-468-656A-5 US-09-468-656A-5 ; Sequence 5, Application US/09468656A ; Sequence 5, Application US/09468656A ; Patent NO. 6582706 ; Patent NO. 6582706 ; GENERAL INFORMATION: ; APPLICANT: Adamou, John E. ; APPLICANT: Adamou, John E. ; TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus ; TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural ; TITLE OF INVENTION: Motifs ; FILE REFERENCE: 469201-444	Oy 1558 ATTAGCTTGATAAGATATCAAGGTCAGATTTGATTATCATGATATAACATGATATTAATTGATAACATGATATTAATTGATAACATGATATTAACATGATATAACATGATATAACATGATATAACATGATATAACATGATATAACATGATATAACATGATATAACATGATATAACATGATAAAAAGA 1679 1618 TGATGAAGGAGATTCCACATATATGACCCATATACCCCTGAATTAAAAAAGA 1688 1629 TAATGAAGGAGATTCCACATATATGACCATATACCCCTGAATTAAAAAAGA 1688 1629 TAATGATCATAAGGAGAAAAACCAAATTCCACATATACCCACTGAATTAAAAAAGA 1688 1629 TAATGATCATAAGAGACCAAAACCAAATCCAACTAACAACAAAACCAATTCCATATATGATTCAA 1857 1629 TAATGATCATCAACAAAAACCAAATCCAACTACAAAACCAAATCCAAATCTCAAATCTCAAATCTCAAATCTCAAATCTCAAATCTCAAATCTCAAATCTCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAAATCCAAAATCCAAAAACCAAAAAA	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 1478; Conserv
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GENERAL INFORMATION:
                                                                                                                                           Matches
                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 65,
                                                                                                                                                                                                                                                                                TELEPHONE: (301) 309-8512
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                       STRANDEDNESS: don TOPOLOGY: linear
                                                                                                                                                                                                                                                 TYPE: nucleic acid
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CITY: Rockville
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9410 Key West Avenue
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TCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAAGCAAGTT 1245
                                                                                                               AGGCCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTC-----TTT
                                                                                                                                                                            TTGGGTACCAGATTCAAGGCCAGAACCAACCAAGTCCACAACCGACTCCGGAACCTAGTCC 1077
                                                                                                                                                                                                                                                                                     AACCGCCAGAGGTGTAGCTGTCCCTCATGGTAACCATTACCACTTATCCCTTATGAACA
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                                                                                                                                                                                                                                       AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCCTTCGTTATCGTTCAAACCA 1017
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                                                           GGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTC 1185
                                                                                             AAGTCCGCAACCTGCACCAAATCCTCAACCAGCTCCAAGCAATCCAATTGATGAGAAATT
                                                                                                                                                            TTGGGTACCAGATTCAAGACCAGAACAACCAAGTCCACAATCGACTCCGGAACCTAGTCC
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RESULT 8
US-09-536-784-65
; Sequence 65, Application
; Patent No. 6573082
; GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 1481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 65: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 41,9
REFERENCE/DOCKET NUMBER: 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE Diskette, 3.50 inch,

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ
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FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
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                        TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTC
                                                                                                                                                                            TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA
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FILING DATE: 30-Oct-1997
CLASSIFICATION: «Unknown»
                                                                         TGCAGCTCATGCGGATAATATTCGGACAAAAGAAGAGATTAAACGTCAGAAGCAGGAACG
                                                                                                               TGAAATCAAGGGTGGTTATGTCATTAAGGTAAACGGTAAATACTATGTNTACCTTAAGGA
                                                                                                                                                                                                                                 CAGTGAAGAGCTCCTCATGAAAGATCCGAATTATCAGTTGAAGGATTCAGACATTGTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2290 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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RESULT 9 US-08-961-527-243 Sequence 243, Application US/08961527 Patent No. 6420135 GENERAL INFORMATION: APPLICATION NUMBER: US/08/
FILING DATE:
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: ZIP: 20850 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett APPLICANT: Charles Kunsch TITLE OF INVENTION: Streptococcus NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: APPLICANT: STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA ADDRESSEE: Human Genome Sciences, US/08/961,527 pneumoniae storage Polynucleotides and

Sequences

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INFORMATION FOR SEQ ID NO: 243:
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMUNICATION INFORMATION:
TELECHONE: (301) 309-8504
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LENGTH: 2359 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6159469
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 181, Application
APPLICATION NUMBER: U
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                             ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                           APPLICANT: Choi et. al
TITLE OF INVENTION: St:
NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
                                                                                                     MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                           STATE:
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TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 1342 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
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                                                AGCAAAAGGATCAACTAGCAAGCCAGCAAATAAATCTGAAAATCTCCAGAGTCTTTTGAA
                                                                             CAACAACAGCAACACTAACAGTCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAA
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US-09-536-784-181
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PATENT NO. 6573082

GENERAL INFORMATION:
APPLICANT: Choi et. al.
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 181:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4M
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION CONTACTOR
PRIOR APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (2013) 309-8504
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CITY: Rockville
STATE: Maryland
                                                                                        TTTGACTCCTGATGAGGTTAGCAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAA 156
                                                                    CTTGACACCAGACCAGGTTAGCCAGAAAGAAGAATTCAGGCTGAGCAAATTGTAATCAA 147
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 AATTACAGATCAGGGCTATGTAACGTCACACGGTGACCACTATCATTACTATAATGGGAA
                         GATAACAGACCAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAA 216
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Pred. No. 3.2e-96;
0; Mismatches 276;
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RESULT 12
US-09-468-656A-7
; Sequence 7, Application US/09468656A
; Patent No. 6582706
; GENERAL INFORMATION:
APPLICANT: Johnson, Leslie S.
APPLICANT: Adamou, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Stru
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-444
CURRENT APPLICATION NUMBER: US/09/468,656A
CURRENT FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1998-12-21
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; SOFTWARE: PatentIn Ver. 2.
; SEQ ID NO 7
; SEQ ID NO 7
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Streptococcus p
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Best Local Similarity
Matches 631; Conserv
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     CCACTTCATCCCTTACTCTCAAATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCC
                                       CCCTGCTAAGATTATCAGTCGTACACCAAATGGAGTTGCGATTCCGCATGGCGACCATTA
                                                             TCCAGCACAAATCACAAGTCGAACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTA
                                                                                                              GGAACTCTATGATTCACCTAGCGCCCAACGTTACAGTGAATCAGATGGCCTGGTCTTTGA
                                                                                                                                  ACAGCTCTACAAACTGCCTTTGAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGA
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Pred. No. 3.3e-96;
0; Mismatches 276;
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US-08-961-527-192/c
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                                                                                                                                                                                                                                                                                 Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (301) 309-851:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Charles Kunsch
TITLE OF INVENTION: Strep:
NUMBER OF SEQUENCES: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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OPERATING SYSTEM: MSDOS version of SOFTWARD
                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                                                                                                      CTTGACACCAGACCAGGTTAGCCAGAAAGAAGGAATTCAGGCTGAGCAAATTGTAATCAA
                                                                                                              AATTACAGATCAGGGCTATGTAACGTCACACGGTGACCACTATCATTACTATAATGGGAA
  TAAAGACGCTGATATTGTCAATGAAGTCAAGGGTGGTTATATCATCAAGGTCGATGGAAA
                     AAAAGATGAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAA 336
                                                                              GGTTCCTTATGACGCTATCATCAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCT
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                                                         AGTTCCTTATGATGCCCTCTTTAGTGAAGAACTCTTGATGAAGGATCCAAACTATCAACT
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9410 Key West Avenue
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Pred. No. 7.4e-96;
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US-08-961-527-355
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                                                                                                                                                                                                                                                                   Sequence 355, Application US/08961527 Patent No. 6420135
                                                                                                                                                                                                                                                         GENERAL
COMPUTER: HP Vectra 486,
OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OFILING DATE:
                                                                                 ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                          APPLICANT: Charles I
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Gen
                                                                                                                                         CITY: Rockville
STATE: Maryland
                                                                                                                           COUNTRY:
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9410 Key West Avenue
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                                                         MSDOS version 6.2
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               US/08/961,527
                                                                                    3.50 inch,
                                                                                                                                                                                  Sciences,
                                                                                                                                                                                                                          pneumoniae Polynucleotides
                                                                                    1.4Mb
                                                                                     storage
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and Sequences

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CAACAACAGCAACACTAACAGTCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAA 816
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                                                                                                                                                                                                                                                                                                                                          GGAACTCTATGATTCACCTAGCGCCCAACGTTACAGTGAATCAGATGGCCTGGTCTTTGA
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CCACTTTATTCCTTACAGCAAGCTTTCTGCCTTAGAAGAAAAGATTGCCAGAATGGTGCC 5786
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                                                                            CCACTTCATCCCTTACTCTCAAATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCC
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RESULT 15
US-08-961-527-258
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; Patent No. 6420135
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US-08-961-527-355
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAC: (301) 309-8512
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
LENGTH: 973 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 77.9
Matches 492; Conservative
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IOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                              GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCT
                                                                                                                                                                                TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA
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77.5%;
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Pred. No. 3.4e-95;
0; Mismatches 131
                                                                                                                                                                                                                                                                                   -AACTCAAGAGCAGATAATGCTGTTGCTGCAGCCAGAGC
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 'PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3: CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Rockville
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                               GCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCACAGTGAAGATCCAAATAAGAACT
                                                                                      ATGCCTATGTAACTCCACATATGACCCATAGCCACTGGATTAAAAAAAGATAGTTTGTCTG
GTAACGCTAGCGACCATGTTCAAAGAAACAAAAATGGTCAAGCTGATACCAATCAAACGG
                                                                                                                                    AGTGGTTTGACGAAGGCCTTTATGAGGCACCTAAGGGGTATACTCTTGAGGATCTTTTGG
                                                                                                                                                                AAGTCAAAAACGGTAGTTTAATCATACCTCATTATGACCATTACCATAACATCAAATTTG
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nilarity 60.3%;
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Pred. No. 4.4e-57;
0; Mismatches 236;
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US-08-743-637B-34/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                            TELEFAX: (414)277-5591
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 841 base pairs
TYPE: nucleic acid
                                                                                                                                          NAME: BAKER, Jean C.
REGISTRATION NUMBER: 85
REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/743,637B FILING DATE: 04-NOV-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: MILWAUKEE
STATE: WISCONSII
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                 TOPOLOGY:
                                  STRANDEDNESS:
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OUELLETTE,
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TE, Marc
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PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
IDENTIFY COMMON BACTERIAL PATHOCENS AND ASSOCIATED
ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
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RESULT 17
US-08-526-840B-34/c
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                                                      TELEFAX: (414) 277-559;
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 841 base pairs
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                      NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE
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STRANDEDNESS: uc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Milwaukee
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                                    nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTACGAAATAATTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAA 2329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGCTTGCGAAAGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGT 2269
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AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
COMMON BACTERIAL PATHOCENS AND ANTIBIOTIC RESISTANCE GENES
FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
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Pred. No. 3e-20;
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RESULT 18
US-08-232-463-14/c
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Best Local Similarity
                                                                                                           FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: DORNER
                                               INFORMATION FOR SEQ ID NO:
              SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F.G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
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ORIGINAL SOURCE:
ORGANISM: Str
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APPLICATION NUMBER:
                                                                                TELEFAX:
                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                      FILING DATE:
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1800 Diagonal Road
                                                                             (703)683-4109
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Pred. No. 3e-20;
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US-09-134-001C-2243
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Best Local Similarity
Whiches 13; Conserva
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; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
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                                                                                                                      *Query Match
Best Local Similarity
Matches 187; Conserv
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                               SEQ ID NO 2243
LENGTH: 11091
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2243, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
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AAATAGTTTÄGATCÄÄATCAATAACTTCAGACCAGÄTTTTAGTAAAAAACGTAATGCAGT
                            AGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGCGAAA----GATTTACC
                                                           AAAAGCCAAAAATGATGTAAATCAATCTCAAACTAATCAGCAAGTTGAAAATGCTGAGCA
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3.4%; Pred. No. 1.5e-05;
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                                                                                                                     Score 51.6; DB 4;
Pred. No. 0.00072;
0; Mismatches 205;
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                                                                                                                    Matches
                                                                                                                                                Query Match
                                                                                                                                                                                                                                                    TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TITLE OF INVENTION: Human Tel
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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CITY: San Francisco
                                                                                                                                    Local Similarity
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ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                           ACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGAGGAAATCA
                                                                                       AAGATGAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAAT 338
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268 Bush Street, Suite 3200
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                                                                                                                    Conservative
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                                                                                                                                  Score 45.2; DB Pred. No. 0.018;
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US-08-676-974-2
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MOLECULE TYPE: US-08-676-974-2
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0
CURRENT APPLICATION DATA:
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NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
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                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 77; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399 ATCGACAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTG 458
                                       459 CTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATG 518
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SNGARGARGAYWSNGAYYTNGARGARWSNGAYWSNATHGAYGAYGGNGARGARYTNGCNC 910
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                                                                                   CNGTNCARATHCARAARMGNGCNGTNAARMGNCCNGCNGCNAARWSNWSNGAYCAYW 850
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ER: UCB96-055
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Query Match
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US-09-098-487-2
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                    RESULT 23
US-08-973-462-2
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Sequence 2, Application US/08973462B
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TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
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APPLICANT: COLLIN
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NAME: OSMAN Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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STRANDEDNESS: double
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CLASSIFICATION:
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Sequence 1, Application US/08973462B
Patent No. 6191270
GENERAL IMPORMATION:
APPLICANT: DRUILHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC ST/FILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION UMBER: ECT/FR96/00894
EARLIER APPLICATION DATE: 1996-06-12
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US-08-973-462-1
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APPLICANT: DAUBERSIES, PIERRE
APPLICANT: DAUBERSIES, PIERRE
APPLICANT: DAUBERSIES, PIERRE
APPLICANTON: MALARIAL PRE-ERYTHROCYTIC STITILE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STITILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06-0894
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER APPLICATION NUMBER: FR 95/07007
EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
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Best Local Similarity
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ORGANISM: P. falciparum
FEATURE:
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LOCATION: (1)
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Pred. No. 0.
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STAGE

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; LENGTH: 696
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-193
                                                                                                                      APPLICANT: Puranam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FO
TITLE OF INVENTION: AND TREATING CONDITIONS, DI
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
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US-09-461-697-193
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; TYPE: DNA
; ORGANISM: P. falciparum
US-08-973-462-1
                                                                          NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 193
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 193, Application US/09461697 Patent No. 6277974
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EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lo, Donald C
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Puranam, Kasturi
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APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND TREATING CONDITIONS,
TITLE OF INVENTION: CELL DEATH
FILL REFERENCE: 10001-005-999
CURRENT APPLICATION UMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 191
LENGTH: 699
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                                                                                                                                                  Sequence 189, Application US/09461697 Patent No. 6277974 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6277974
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Furanam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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APPLICANT: Lo, Donald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2042
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                                                                                                                                                                                                                                                                                                            CAAGTAGAGACTGAAAAAGTAGAAGCCCCAACTCAAAGAAGCAGAAG
                                                                                                                                                                                                                                                                                                                                                          GTAAAAGTCAAAGAAGATGAAAAAGAGAGAGAGATGGAAAAGAAGATGAAGGTGGAAAT
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Pred. No. 0.13;
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                                                                                                                                                                                                                                                                                  ; TYPE: DNA; Homo sapiens US-09-461-697-187
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CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 189
LENGTH: 717
                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILLING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 187
LENGTH: 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 187, Application US/09461697 Patent No. 6277974
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Best Local Similarity
Matches 88; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Puranam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR I
TITLE OF INVENTION: CELL DEATH
TITLE OF INVENTION: CELL DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICAW: ---,
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT. Portbury, Stuart D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: COGENT NEUROSCIENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING TITLE OF INVENTION: CELL DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                         2042
                                 2162
                                                                                                 2102 AAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCT
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Puranam, Kasturi
                             CAAGTAGAGACTGAAAAAGTAGAAGCCCCAACTCAAAGAAGCAGAAG 2207
                                                                 GGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAGACCACAGTGAAGATCCAAAT 2101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lo, Donald C
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                                                                                                                                                                                                           Score 41.2; DB Pred. No. 0.13; 0; Mismatches
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 Length 774;

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APPLICANT: Lo, Donald C.

APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Ext., Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISE
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
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US-09-220-132-155
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                                                                                                                       US-09-220-132-155
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                                                                                                                                                                          SOFTWARE: Fas
SEQ ID NO 155
LENGTH: 1280
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LENGTH: 819
TYPE: DNA
                                        Best Loc
Matches
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Patent No. 6277974
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6506607
GENERAL INFORMATION:
                                                                                                                                                                                                                               APPLICANT: Shyjan, Andrew W.

TITLE OF INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CAN
FILE REFERENCE: 07334-074001
CURRENT APPLICATION NUMBER: US/09/220,132
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 155,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                        Local Similarity
mes 88; Conserv
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  2162 CAAGTAGAGACTGAAAAAGTAGAAGCCCCAACTCAAAGAAGCAGAAG 2207
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                                                                                                                                                                                                                     FastSEQ for Windows Version 4.0
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                                          Conservative
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53.0%;
                                                        1.7%;
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                                      Score 41.2; DB Pred. No. 0.17; O; Mismatches
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                                        78;
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                                                                             Length 1280;
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US-09-461-697-184
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-184
                                                                                                                                                                                                                                                                                                                                                                              RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Watanam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REPERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT APPLICATION NUMBER: US/09/461,697
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 184
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          SEQ ID NO 21
LENGTH: 5340
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                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/09627122
Patent No. 6472521
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                                                                   FILE REFERENCE: 02481.1678
CURRENT APPLICATION NUMBER: US/09/627,122
CURRENT FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                   APPLICANT: Schwerdel, Marc
TITLE OF INVENTION: OLIGONUCLECTIDES
TITLE OF INVENTION: EXPRESSION
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                                                         SOFTWARE:
TYPE: DNA
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Local Similarity 53.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2102 AAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCT
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                                                       PatentIn Ver.
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Thomas, Mary Beth
                                                                                                                                                                                                                                                       Uhlmann,
Greiner,
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Unger, Eberhard
Gothe, Gislinde
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-601-198-56
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US-09-601-198-56/c
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GENERAL INFORMATION:
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Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cassell, Gail H.
APPLICANT: Chen, Ellson Y.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Elliot
TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
TITLE OF INVENTION: UREALYTICUM
FILE REFERENCE: UAB-13452/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/073,189
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 181.
SOPTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/601,198
CURRENT FILING DATE: 2000-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Ureaplasma urealyticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 14066
                                    2319
                                                                                                                                                         2669
                                                                                                                                                                                                2199
2549 TAATTACTGAAACTGGAAATCCGGTTTTTAAAAGTTATTCAAACTCAAAATGATACTA 2493
                                                                                                                                                                                                                                                                          2139 CACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGAAAAGTAGAAGCCCAACTCAAAG 2198
                                                                                                                                                                                                                                                                                                                                                      2079 AAGACCACAGTGAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAA 2138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        680 TACTTGGAAGTTAAAAATACCTTGATGAAAGAGATAGAACAAATTACAACAACACATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 CTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGAGGGTCAAGGGT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      740 GATCAAGGTGATCATCATAATTATCTTTATAATGATGATGATATCATAAGACAAAATTTA 681
                              CAGAAGCAGAAAATTACTTGCGTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTA 2375
                                                                             AACCATTAAAAACTCACACTAATTTATCTGTATCGATTAATGATAAAGAAAATATAAGTT 2550
                                                                                                                                                       GTCAAATCGATAATTTAAATCCAGAAACTAAATATAAATTAGAAAATATTGAATTAAGTA 2610
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                                                                                                                CTCTAGCTGGTTTACGAAATAATTTGACTCTTCAAATTATGGATAACAATAGTATCATGG 2318
                                                                                                                                                                                              AAGCAGAAGTTTTGCTTGCGAAAGTAACGGATTCTAGTCTGAAAGCCCAATGCAACAGAAA
                                                                                                                                                                                                                                       AAGATGATAATGATGTTTTAAATAACATTGATGCAACTGTTAAATTTAAAGATGAACATA 2730
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 4; Length 14066; Pred. No. 0.67;
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Pred. No. 0.41;
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Gaps

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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUITITIE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND FILE REFERENCE: GTC-007

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR PILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-13

PRIOR PILING DATE: 1997-08-14

VINNEROR PILING DATE: 1997-08-14

SEQ ID NO 925

LENGTH: 1704

LENGTH: 1704

TYPE: DNA
                                                                                                                                                                                                                US-09-328-352-2472

Sequence 2472, Application US/09328352

Patent NO. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AN
FILE REFERENCE: GTC99-03PA
                                                             ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2472
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Query Match
Best Local Similarity
                                                                                                                      SEQ ID NO 2472
LENGTH: 792
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                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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  40.2;
No. 0
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US-09-134-001C-322
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GENERAL INFORMATION:
APPLICANT: LYNN DOUGETTE-Stamm et al
APPLICANT: LYNN DOUGETTE-STAMM et al
TITLE OF INVENTION: UCCLEIC ACID AND AMINO
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNO
FILE REFERENCE: GTC-007
CURRENT APPLICATION UNMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 112; Conserv
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LENGTH: 30549
                                                                                                                                              Sequence 1027, Application Patent No. 6380370
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CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER: OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                 GTAGAGCAAGCACTCAGTGAATTGAACAACGCCAAATCAGCGCTTAGAGCTGATAAACAA
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Pred. No. 1.
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                                                              AMINO ACID SEQUENCES RELATING DIAGNOSTICS AND THERAPEUTICS
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                                                                                    STAPHYLOCOCCUS
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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1027
LENGTH: 297
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
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                                                                                                                                                                                                                                                                                                                                                ; LENGTH: 1716
; TYPE: DNA
; ORGANISM: Staphylococcus
US-09-134-001C-1028
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                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1028, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 110;
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                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: MUCLEIC ACID AND
TITLE OF INVENTION: EPIDERMIDIS FOR
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1997-11-08
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                                                                                                                                                                                                                                                                                               Match 1.7%;
Local Similarity 48.5%;
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Local Similarity 48.5%;
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1502
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                                                                                                                                                                                                                                            1704 CAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTTA 1763
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                                                                     AAAGTACACAAGATGATAATGATAATCAAAATACGCAACAAGGTAATACTAAACAAAAACA
                                                                                                                                        ATTTGATTATTCCTCATAAGGATCATTACCATAATATTAAATTTGCT 1930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGATCAAGCCGGTGCTACGGTTAAACCTGGATCTGCTCCAAATCAAGACGCTGAAGCAA
ATCAAAATGCTGAACAAGGTAATACTGGCGGTACAGATAAAGATGCT 1548
                              ATTTGATTATTCCTCATAAGGATCATTACCATAATATTAAATTTGCT 1930
                                                                                                                                                                                                             CTGATCAAGCCGGTGCTACGGTTAAACCTGGATCTGCTCCAAATCAAGACGCTGAAGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGTACACAAGATGATAATGATAATCAAAATACGCAACAAGGTAATACTAAACAAAACA
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                                                                                                                                                                                                                                                                                                                                                                  epidermidis
                                                                                                                                                                                                                                                                              Score 39.8; DI
Pred. No. 0.49,
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMINO ACID SEQUENCES RELATING DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                               0.49;
                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                              117;
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PATENT NO. 6503729
PATENT NO. 6503729
PATENT NO. 6503729
PATENT OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1998-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                   US-08-916-421B-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
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CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/073,189
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cassell, Gail
APPLICANT: Chen, Ellson
APPLICANT: Glass, Jennif
                                                                                                                                                                                                                                                                                                              APPLICANT: Bult et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Heiner, Cheryl R. APPLICANT: Lefkowitz, Elliot TITLE OF INVENTION: NUCLEIC ACID TITLE OF INVENTION: URBALYTICUM FILE REFERENCE: UAB-13452/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                    LENGTH: 1
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Ureaplasma urealyticum
ORGANISM: Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1202 АЛАGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGT 1261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAATTTTAGGGGAAGTTAATTT 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACATTAGAAAGTAAAGTAGATGATTATACAATAATGTTTCTAACCAACTAATTCAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glass, Jennifer S
Glass, John I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                         of the Methanogenic Archaeon, Methanococ
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LOCATION: (31200...
LOCATION: (31200...
OTHER INFORMATION: n er
OTHER INFORMATION: n er
NAME/KBY: misc feature
NAME/KBY: (312993)...(3 LOCATION: (312993)..(312993) OTHER INFORMATION: n equals OTHER INFORMATION: n equals OTHER INFORMATION: n equals VAME/KEY: misc_feature \.OCATION: (98343) ... (98343) \.THER INFORMATION: n equals a, VAME/KEY: misc_feature COCATION: (98239)..(98239)

THER INFORMATION: n equals NAME/KEY: misc_t OCATION: (84812)..(84812)
OTHER INFORMATION: n equals OCATION: (84808) .. (84808)
OTHER INFORMATION: n equals OCATION: (84773)..(84773)

OTHER INFORMATION: n equals COCATION: (28257)..(28258)
OTHER INFORMATION: n equals EATURE:
NAME/KEY: misc_feature
LOCATION: (28222) ... (28222)
OTHER INFORMATION: n equals a, OCATION: (103998)..(103998) THER INFORMATION: n equals IAME/KEY: m OCATION: (98159)..(98159) NAME/KEY: misc AME/KEY: misc THER INFORMATION: n equals AME/KEY: misc OCATION: (2342 OCATION: (191995)..(191995)
THER INFORMATION: n equals a, OCATION: (191989)..(191989)
THER INFORMATION: n equals THER INFORMATION: n equals AME/KEY: mi AME/KEY: m: CATION: (231980)..(231980) THER INFORMATION: n equals AME/KEY: m THER INFORMATION: n equals THER INFORMATION: n equals a, ER INFORMATION: n equals ER INFORMATION: n equals ER INFORMATION: n equals 180 28 12837)..(31201 ANTION: n equals a, feature reacure teature feature reature feature eature (98120)(98266) (234187)(148948) (309418)(231980) (163385) (234220)a ' a a a a, a a a ' a ' a, b) a, a, a, gı Y a, a, ā, a a, Ĺ t, Ĺ ŗ ŗ Ĺ 'n Ĺ , ļ Ĺ Ĺ 'n ή 'n ŗ Ĺ ή, Ĺ ۲ ņ c, C, ņ ņ C, ū ç Ç 'n ņ ņ 'n G ņ ņ Ç ņ ú 'n 'n 'n ņ 'n or P 9 ç g õ ç õ or ဝူ or 9 9 ဝူ ğ or õ õ 9 9 g 9 9 or ۵ ω ω ω ω ω ω ω ω ω ω g

LOCATION: (1310988) .. (1310988)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (1313224) .. (1313224) NAME/KEY: misc_feature LOCATION: (1470091)..(1470091) OTHER INFORMATION: n equals a, OTHER INFORMATION: n equals OTHER INFORMATION: n equals LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, OTHER INFORMATION: n NAME/KEY: misc_featur LOCATION: (1119881)..(1119881) OTHER INFORMATION: n equals a, LOCATION: (1096846)..(1096846) OTHER INFORMATION: n equals a, NAME/KEY: misc_ OTHER INFORMATION: n equals a, OTHER INFORMATION: n equals a, OTHER INFORMATION: n equals NAME/KEY: misc_feature NAME/KEY: misc_feature NAME/KEY: misc_feature OTHER INFORMATION: n equals a, LOCATION: (674435)..(674435) OTHER INFORMATION: n equals NAME/KEY: misc_feature OTHER INFORMATION: n NAME/KEY: misc LOCATION: (1349 OTHER INFORMATION: n equals a, LOCATION: (779455)..(779455) THER INFORMATION: n equals OTHER INFORMATION: n equals DTHER INFORMATION: n OTHER INFORMATION: n NAME/KEY: misc_ LOCATION: NAME/KEY: misc NAME/KEY: misc INFORMATION: n equals INFORMATION: n equals (1130881) .. (1130881) misc (1349491) . . (1349491) (855539)..(855539) (1349473)..(1349473) RMATION: n equals a, (1084830) . (1084830) (600992) . . (600992) feature teature feature feature feature feature feature feature feature teature feature feature feature feature feature feature)..(657081))..(871619))..(713652))..(682442) .. (622708 (779676) (657203) equals a, equals a, equals equals equals equals (559167) a, a a, a, a, es (e) b O a, a a D) ŗ Ţ ή, Ļ , ή, ŗ ļ 'n , , Ç r ŗ (1 , ļ, ļ , 'n , ņ ú ņ 'n ņ ņ 'n ņ ú û ņ ņ ņ ņ ņ ú 'n ů, ç or or P 9 or or or or or ဝူ õ õ ç or g 20 õ ç or C ö or or 2 9 9

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RESULT 41
US-09-671-317-14/c
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                                                                                                                                                   FILE REFERENCE: 62.US3.CIP
CURRENT APPLICATION NUMBER: US/09/671,317
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 09/536,178
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: PCT/IB00/00403
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 1999-03-25
PRIOR FILING DATE: 1999-03-25
                                                           SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/09671317 Patent No. 6528260
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Best Local
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                                                                                         PRIOR APPLICATION NUMBER: US 60/131,961
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 977
                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM FILE REFERENCE: 62.US3.CIP
                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                               SOFTWARE:
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LOCATION: (1664854)..(1664855)
OTHER INFORMATION: n equals a,
LENGTH: 929
TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1637998)..(1637998)
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LOCATION: (1603734)..(1603734)
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                                                                             Patent.pm
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Bougueleret, L
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                                                                                                                                               NUMBER: US 60/126,269
1999-03-25
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Pred. No. 21;
0; Mismatches 211; Indels
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1191
SEQ ID NO 1191
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Best Local Similarity
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                                                                                                                                                                                                                         ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-1191
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US-09-134-001C-1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1191, Application US/09134001C Patent No. 6380370
                                                                                                                                           Matches 105;
                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 674..679,881..882,892..893
OTHER INFORMATION: n=a, g, c or t
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LOCATION: 481.500
OTHER INFORMATION: 12-454-363.misl,
NAME/KEY: misc_binding
LOCATION: 502.521
OTHER INFORMATION: 12-454-363.mis2,
                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 501
OTHER INFORMATION: 12-454-363 : polymorphic base A or
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LOCATION: 139..158
1573 TACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGATGAAGGAGATGC 1632
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                                                                                                   AAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATTAGCTGATAAGTA 1572
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                                                            AAGTATTGAAGCTAAAATAGGTGAAGAAGAAAAATTTAAAAGGTCATCTTGGAGAAAGTGC 197
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Pred. No. 0.84;
0; Mismatches 11
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                                                                                                                                                                                Length 1839;
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RESULT 43
US-08-360-606B-29
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US-08-360-606B-29
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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (312)913-000: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1856 base pairs
TYPE: nucleic acid
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SOFTWARE: MS WORD 7.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Robert P. Peery
TITLE OF INVENTION: Methods and Reagents for
TITLE OF INVENTION: Detecting Fungal Pathogens in
TITLE OF INVENTION: Biological Sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Berghoff, Paul H.
REGISTRATION NUMBER: 30,243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                        1396
                                                                                                                                                                                        1276 ААСТЭСТАЛАЛАЛАЛАЛАТЭТТЭСТССТСЭТЭЛССАЛЭЛАТТТТАТЭЛТАЛАЛЭСАТАТАЛ 1335
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   AGATGTTTTAAAAAGATTCCCACAAGGTAATGGTATATTATATGATTTTAGAATTTTTAGA
                                    AGCCTTAGACAAATTATTAGAACGCTTGAATGAATGAATCGACTAATAAAGAAAAATTGGT 1455
                                                                           CCCATTAATTCATGAACATATTCAATTTGCTCATTGTTATAAAGATCAAGCTGGTTGGCA
                                                                                                              TCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCGTAATTCTGATTTCCA 1395
                                                                                                                                                   AACTGCTCCTAAAGAGAATTATTTTTGGTTTAAAAGAATTACCTGAAAATGAAACTTT
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7: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAGCCTTTCTGATAA 1692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08360606E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jnanendra K. Bhattacharjee
Richard C. Garrad
Paul L. Skatrud
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae
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                                                                                                                                                                                                                           Score 38.8; DB Pred. No. 0.96; Mismatches
                                                                                                                                                                                                                                                                DB 2; Length 1856;
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US-08-861-464-13
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US-08-861-464-13/c
                                                           Matches
                                                                           Query Match
Best Local
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                            NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 15-AUG-
FILING DATE: 15-AUG-
PRIOR APPLICATION DATA: 1
APPLICATION NUMBER: 1
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/861,464
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Guarente, Leonard P. APPLICANT: Austriaco Jr., Nicanor APPLICANT: Kennedy, Brian
                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
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                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                      TOPOLOGY:
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2090 GAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAG 2149
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VENTION: Genes Determining Cellular Senescence
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                                                                        Score 38.8;
Pred. No. 1;
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                                                        Mismatches
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US-08-396-001-13
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US-08-396-001-13/c
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SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Austriaco Jr., Nicanor
APPLICANT: Claus, James
APPLICANT: Cole, Francesca
APPLICANT: Kennedy, Brian
TITLE OF INVENTION: Genes Determining
TITLE OF INVENTION: Yeast
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                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2150 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                                                                                                                                            Local
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5. 5919618
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                                                                                                                                                                                                                            Similarity
 TGGGTTGCGGAAGAAGTTGACACGACAGTAGATGTTGGAGCAGCTTCTTCACTAGATG
                                  TTGCTTGCGAAAGTAACGGATTCTAGTCTGAAAGCCCAATGCAACAGAAACTCTAGCTG
                                                                      GTAGAAGTAGATGGAAGTGGAAGAAGTACTAGATTTAGTGGCAGAAGAAGCACTAGAT
                                                                                                     CCAGAAGTCCCTCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGGAAGTT
                                                                                                                                         GAAGAAGAAGAAGAGGAGGAAGAAGAAGAAGAAGTAGAAGTAGAAGTAGAA
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N: .435
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Pred. No. 1;
0; Mismatches
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US-09-323-433A-13/c
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CURRENT FILING DATE: 199-06-01
PRIOR APPLICATION NUMBER: US 08/396,001
PRIOR FILING DATE: 1995-02-28
PRIOR APPLICATION NUMBER: PCT/US94/09351
PRIOR APPLICATION NUMBER: US 08/107,408
PRIOR APPLICATION NUMBER: US 08/107,408
PRIOR FILING DATE: 1993-08-16
PRIOR FILING DATE: 1993-08-16
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                                                                                                                                                                                                                                                                                                                                                                    sequence 2, Application US/08119125A Patent No. 5610011
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APPLICANT:
APPLICANT:
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NAME/KEY: CDS
LOCATION: (563
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NUMBER OF SEQ ID NOS:
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (563)...(1987)
OTHER INFORMATION: SAG1
                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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COMPUTER : Diskette, 3.5
MEDIUM TYPE: Diskette, 3.5
COMPUTER: IBM compatible
COMPUTER: IBM compatible
                                                                                                                                                                                                                                                                                                                 APPLICANT: SMITH, APPLICANT: VECHT,
                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                       STATE:
                                                                                                                                                         STREET:
                                                                                               COUNTRY: The Netherlands
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Claus, James J.
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VECHT, Uri
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                                                                                                                                                                                                                                  DNA Sequences which code for Virulence Characteristics of Streptococcus suis and parts thereof, polype antibodies derived therefrom and the use thereof for the diagn protection against infection by S. suis in mammals, including a
                                                                                                                                                                            Diergeneeskundig Instituut
                                        3.50 inch,
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SOFTWARE: WordPerfect v. 6.0 CURRENT APPLICATION DATA:

FILING DATE:

20-SEP-1993

US/08/119,125A

APPLICATION NUMBER:

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Matches
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Best Local Similarity
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APPLICATION NUMBER: PCT/I
FILING DATE: 19-MAR-1992
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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Nucleic acid with corresponding amino acids
DEDNESS: single stranded
GATGAGAAGGAATCAGCTAAGAATGCAGTGGAAGAGGCGGCTAAGGTAGCAACAGCCGCT 3660
                                                       AAAGCGGATGAAGAGCCAGTAGAGGAAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAG
                                                                                                                        ATTGCCAAAGAAGCAGAATCAGCTAAGAAAGCGATTGACGACAATCCAAACTTGACTCCA 3600
                                                                                                                                                                                   AATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCACAGTGAAGATCCAAATAAGAACTTC 2110
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 dyad symmetry regions from bp 6631 to 6644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    start of repetitive units R1-R11 bp 2869, 3097, 3292, 3520, 4087, 4381, 5065, 5293, 5521:
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bp 89 to 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dyad symmetry regions from bp 6554 to 6566 and
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bp 361 to 498
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bp 176 to 181
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bp 66 to 71
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                                                                                                                                                                                                                                                                              1.6%;
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Pred. No. 2
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Mismatches 169;
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GGAGAATTTGACTCCTGATGAGGTTTAGCAAGCGTGAAGGAATCAATGCTGAGCAAATCGT 150

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                                                        Query Match 1.6
Best Local Similarity 46.0
Matches 131; Conservative
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                                                                                                                                         TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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CTTY: Arlington
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                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                          TELEPHONE: 703-816-4100
                                                                                                                                                                                                                                                                                                                     NAME: Mitchard, Leo REGISTRATION NUMBER:
                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 06-Jul-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                        AACGGTTAAGGAAAATAATCGTGTTTCCTATATAGATGGAAAACAAGCGACGCAAAAAAAC 90
                                                                                                                                                                                 mucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGCGTTGTTAAAA 2350
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AATAGGGAATAATAAAAATATGGATATGTATTTATCTAAGGAAAAAAGTATATCTAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flores, Maria V
O'Sullivan, William J
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                                                                                                                                                          SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphate synthetase
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                                                          Score 38.6; DB 2;
Pred. No. 2.4;
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RESULT 50
US-08-169-927-1
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US-09-150-741-1
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               GENERAL INFORMATION:
APPLICANT: Carl, M
APPLICANT: Dobson,
APPLICANT: Ching, 1
                                                                                          Patent No. 5783441
                                                                                                         Sequence
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APPLICANT: Stewart et al.
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Patent No. 6183996
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TITLE OF INVENTION: Synthetase II
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EARLIER FILING DATE: 1993-12-02
EARLIER APPLICATION NUMBER: 08/446,855
EARLIER FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT FILING DATE: 1998-99-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 8920
TYPE: DNA
ORGANISM: Plasmodium falciparum
 APPLICANT:
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                                                                                                                                                                                                       TAAGATGAAAGAGTTAATAGATAACGAAAATTTAAATGATGAATATAATAATAATGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                CATCAAGATAACAGACCAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAA 210
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                                                                                                             Application US/08169927
                                                                                                                                                                                                                                           TAAGCTAAAAGATGAGGATATTGTTAATGAGGTCAAGGGTGGATA, 315
                                                                                                                                                                                                                                                                                                                     TGGTAAGGTTCCTTATGACGCTATCATCAGTGAAGAATTACTCATGAAAGATCCAAACTA
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             Dobson, Michael E
Ching, Wei Mei
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Mismatches 154;
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TELEFAX: (301) 295-102
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                    PUBLICATION INFORMATION:
AUTHORS: Carl, M.
AUTHORS: Dosson, M. E.
AUTHORS: Ching, W. M.
AUTHORS: Dasch, G. A.
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FRAGMENT TYPE: i
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
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NUMBER OF SEQUENCES:
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NAME/KEY:
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APPLICATION NUMBER: US 0
FILING DATE: 08/09/91
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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NAME/KEY:
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STRAIN: B
                                                                          TITLE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                             JOURNAL:
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STRANDEDNESS: double
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RELEVANT RESIDUES IN SEQ ID NO:
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Bethesda
                1990
                          Characterization of the gene encoding the protective S-layer protein of Rickettsia prowazekii; presence of a truncated identical homolog in rickettsia typhi proc. Natl. Acad. Sci. U.S.A.
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Search completed: November 14, 2003, 01:12:36
Job time: 179 secs
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                                                                      1761 TTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTA 1796
                                                                                                                                             1187 GTATTATTGAATTGAACACTGCAGCAGTAGCTGGTAAACTTATCTCTCTTGGAGGTGCTG 1246
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Title:
Perfect score:
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2389
1 TTCTTACGAGTTGGGACTGT....
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2: \(\cgn2_6/\)ptodata/2/\(\pu\)pna/USO7_NEW_PUB.seq:*
3: \(\cgn2_6/\)ptodata/2/\)pubpna/USO6_PUBCOMB.seq:*
4: \(\cgn2_6/\)ptodata/2/\(\pu\)pna/USO6_PUBCOMB.seq:*
5: \(\cgn2_6/\)ptodata/2/\(\pu\)pna/USO6_PUBCOMB.seq:*
5: \(\cgn2_6/\)ptodata/2/\(\pu\)pna/PCTUS_PUBCOMB.seq:*
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16: \(\cgn2_6/\)ptodata/2/\(\pu\)pna/USO0_PUBCOMB.seq:*
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US-09-452-599-34
Sequence 34, Appl Sequence 2179, Appl Sequence 2019, Appli Sequence 20619, Appli Sequence 20619, Appli Sequence 1597, Ap Sequence 1597, Ap Sequence 15808, A Sequence 2722, Appli Sequence 2722, Ap Sequence 2722, Ap Sequence 2734, App Sequence 2534, App Sequence 193, App Sequence 1946, App Sequence 195, App Sequence 187, Appli Sequence 187, Appli Sequence 188, App Sequence 1893, App Sequence 1894, App Sequence 1894, App Sequence 1893, App Sequence 1619, App Sequence 2535, Ap Sequence 2536, App Sequence 2537, App Sequence 2734, App Sequence 2745, Appli Sequence 2755, Ap Sequence 2757, Ap Sequence 4612, Appli Sequence 4757, Ap Sequence 4757, Ap
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Query Match Best Local Similarity 100.0%; Score 2388; DB 9; Length 2389; Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60	TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 TELEPHONE: (301) 309-8512 INFORMATION FOR SEQ ID NO: 55: SEQUENCE CHARACTERISTICS: LENGTH: 2389 base pairs TYPE: nucleic acid TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 55: US-09-765-272-55	FILING DATE: 22-Jan-2001 CLASSIFICATION: <unknown> PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/961,083 FILING DATE: <unknown> ATTORNEY/AGENT INFORMATION: NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: 36,373 REFERENCE/DOCKET NUMBER: 36,373</unknown></unknown>	ZIF: 20850 ZIF: 20850 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION NUMBER: US/09/765,272 APPLICATION NUMBER: US/09/765,272	APPLICANT: Choi et. al. TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452 CORRESPONDENCE ADDRESS: ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COLUMNEY. High	ALIGNMENTS RESULT 1 US-09-765-272-55 ; Sequence 55, Application US/09765272 ; Parent No. US20020061545A1 ; GENERAL INFORMATION:	c 90 39.2 1.6 462 9 US-09-864-761-3829 Sequence 3829, Ap c 91 39.2 1.6 1074 9 US-09-861-451A-49 Sequence 49, Appl 92 39.2 1.6 1495 12 US-10-032-585-6091 Sequence 6091, Ap 93 39.2 1.6 6944 14 US-10-172-086-111 Sequence 111, Appl 94 39 1.6 477 9 US-09-864-761-5436 Sequence 111, Appl 1 US-10-086-510 Sequence 111, Appl 1 US-10-086-510 Sequence 111, Appl 1 US-09-294-093B-1831 Sequence 131, Appl 1 US-09-294-093B-1831 Sequence 314, Appl 1 US-09-864-761-18737 Sequence 314, Appl 1 US-09-864-761-18737 Sequence 18737, Appl 1 US-09-864-761-18737 Sequence 18737, Appl 1 US-09-864-761-18737 Sequence 137, Appl 1 US-09-8
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Sequence 3, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptcoccus Antigens
FILE REFERENCE: 055190-0044
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
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SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENCTH: 2523

TYPE: DNA

ORGANISM: Streptococcus pneumoniae
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RESULT 3
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Sequence 4, Application US/09884465A
Publication No. US20030077293A1
; GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Brodeur, Bernard
APPLICANT: Brodeur, Bernard
APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptcocccus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
INMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 4

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Oy 1969 TACCTTGGAACATTTGCTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGACGATCC 2028	9 4	Qy 1849 TATGGTTGAGCATACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCA 1908	Qy 1789 AGCAGCTATTTACAATCGTGTGAAAAGGAAAAACGAATTCCACTCGTTCGACTTCCATA 1848	9 4	1669 TGGAAAAGATAGCCTTTCTGATAAGGAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAA	QY 1609 TATAATCAGTGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGAT 1668	0 4	QY 1489 CCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCG 1548	1429 1544	1369 AAATAAGGTGGTAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAAGGCTTGAATGA	1309 CCAGGARITITATGATHAAGCATATAATCTGATAACTGAGGCTCATHAAGCCTTGTTTGN	1249 AAAACAAGAAGTGTTTCACACACTTTAACTGCTAAAAAAAA	1189 1304	1129 TAGICAGCIGGIACGAAAGITIGGGAAGGAIGITATIGIATITGAAGAAAAGGGCATCTCTCG	1081 CCCGCAACCTIGCACCAAAICTTAAAATAGACTAA	1021 GGTACCAGATTCAAGGCAGAGCAAGTCACAACCGACTCCGGAACCTAGTCCAGG	961 GTCTGAATTGGAAGAACGAATCGCTCGTATATTCCCCCTTCGTTATCGTTCAAACCATTG

Best Local Similarity Best Local Similarity Matches 1623; Conser Oy 1 TTCTTACGA	RESULT 4 US-09-769-787-206 Sequence 206, Application US// Publication No. US20030091577; GENERAL INFORMATION: APPLICANT: Microbial Technic: APPLICANT: Gilbert, Christol APPLICANT: Gilbert, Christol APPLICANT: Hansbro, Philip FILLE OF INVENTION: Proteins FILE REFERENCE: PWC/P21129WO CURRENT FILING DATE: 2001-0 PRIOR APPLICATION NUMBER: GB PRIOR APPLICATION NUMBER: US PRIOR APPLICATION NUMBER: US PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-03-1 INUMBER OF SEQ ID NOS: 388 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 206 LENGTH: 2481 TYPE: DNA ORGANISM: Streptococcus pne: US-09-769-787-206	Db 2144 GCAT OY 2089 TGAAN OY 2089 TGAAN OY 2126 Db 2264 GGAAN OY 2126 Db 2324 AGAGG OY 2179 AGTAN Db 2384 GGTT OY 2239 GAAAN OY 2239 GAAAN OY 2239 GGATO OY 2259 GGATO
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GGACAACAATACTATTATGGCAGAAGCTGAAAAACTATTGGCTTTATTAAAGGAGAGTAA
                               GGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGCGTTGTTAAAAGGAAGTAA 2358
                                                                                                        CAAGTCCAATGCCAAAGAGACTCTCACAGGATTAAAAAATAATTTACTATTTGGCACCCA
                                                                                                                                                            GAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAATTTGACTCTTCAAATTAT
                                                                                                                                                                                                                                                                           AGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAAAGTAACGGATTCTAGTCT
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                                                                                                                                                                                                                                                                                                                                                                                      ---AGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGAAAA 2178
                                                                                                                                                                                                                                                                                                                                                                                                                                             TGAGGAAGAACCCCTCGAGAAGAGAAACCGCAAAGCGAGAAACCAGAGTCTCCAAAACC 2237
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RESULT 5
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; Sequence 65, Application US/09765272
; Patent No. US20020061545A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/961,083 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
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STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                  TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAACTTGACACCAGATGAAGTCAG
                                                                                                                                                                                                                                                                                                          CTATATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG
                    TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA
                                                                                        CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA
                                                                                                                                          GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTTCCTTATGATGCCATCAT
                                                                                                                                                              CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT
                                                                                                                                                                                                            TAAGAGGGAGGGGATCAACGCCGAACAAATNGTNATCAAGATTACGGATCAAGGTTATGT
                                                                                                                                                                                                                                             CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
TGAAATCAAGGGTGGTTATGTCATTAAGGTAAACGGTAAATACTATGTNTACCTTAAGGA
                                                                    CAGTGAAGAGCTCCTCATGAAAGATCCGAATTATCAGTTGAAGGATTCAGACATTGTCAA
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REGISTRATION NUMBER: 36,373
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OPERATING SYSTEM: MSDOS version 6.2
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Pred. No. 2.9e-225;
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                           TGATGAATCGACTAATAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAAT 1485
                                                                                          TGNAAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAA
                                                                                                                                                  TGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTT
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                                                                                                                                                                                                                                                                                                                                                       GGTTAGTCAGCTGGTACGAAAAGTTGGGGAAAGGATATGTATTCGAAGAAAAGGGCATCTC
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APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
FITTLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTMARE: PatentIN versi*
SEQ ID NO 5
LENGTH: 26°°
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US-09-884-465A-5
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Qy	Q Q	Qy Db	D Qy	₽ Q	g Qy	D Qy	Qy	QУ	Db Oy	Db Qy	ОУ	Db Qy	D Q	d Qy	D Qy	B 8	Query Best I Matche	; TYPE ; ORG <i>P</i> US-09-88
AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCCTTCGTTATCGTTCAAACCA 1	AACAGCTAGAGGTGTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCCTCA		778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 837	718 TTCTGTAAGCAATCCAGGAACTACAAATACTAACAGCAAGCA	658 AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717	598 GTTATCAGCTAGCGAGTTGGCTGCAGAAACCCTTCCTATCTGGTCGAGGAAATCTGTC 657	538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597	478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537	418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCCTTGGCACGTTC 477	358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAAATCAATC	298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357	238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA 297	178 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237	118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177	58 CTATATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGGTTAG 117	1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTC 57	Query Match 41.1%; Score 980.8; DB 11; Length 2639; Best Local Similarity 67.8%; Pred. No. 1.3e-223; Matches 1473; Conservative 0; Mismatches 638; Indels 60; Gaps 5;	TYPE: DNA ORGANISM: Streptococcus pneumoniae -09-884-465A-5
Qy	Db Qy	gb Qy	Db QY	ם אם עץ	D B CY	B &	5, B &	D &	₽ \$? B &	P &	S B 8	g dy	da da	S B 8	S B &	? B &	DЬ
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Patent No. US20020061545A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 181:
SEQUENCE CHARACTERISTICS:
LENGTH: 1342 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/961,083
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REGISTRATION NUMBER: 98340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
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TITLE OF INVENTION: Streptococcus pneumoniae
NUMBER OF SEQUENCES: 452
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208
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AGTTCCTTATGATGCCCCTCTTTAGTGAAGAACTCTTGATGAAGGATCCAAACTATCAACT
                               GGTTCCTTATGACGCTATCATCAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCT
                                                                        MATTACAGATCAGGGCTATGTAACGTCACACGGTGACCACTATCATTACTATAATGGGAA
                                                                                                            GATAACAGACCAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAA
                                                                                                                                                 CTTGACACCAGACCAGGTTAGCCAGAAAGAAGGAATTCAGGCTGAGCAAATTGTAATCAA
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OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
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Pred. No. 1.4e-81;
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267
                                             APPLICANT: Microbial Technics Limited
APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PMC/P21129WO
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR APPLICATION TUMBER: US 60/125164
PRIOR FILING DATE: 1999-03-19
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US-09-769-787-246
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                                                                                                                                                                                                                                                             Sequence 246, Application US/09769787 Publication No. US20030091577A1 GENERAL INFORMATION:
SOFTWARE: PatentIn
SEQ ID NO 246
                                 NUMBER OF SEQ ID NOS: 388
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; LENGTH: 1455
; TYPE: DNA
; ORGANIEM: Streptococcus
US-09-769-787-246
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                    CCACTTTATTCCTTACAGCAAGCTTTCTGCCTTAGAAGAAAAGATTGCCAGAATGGTGCC
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Pred. No. 1.5e-81;
0; Mismatches 276;
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APPLICANT: Wells, Jeremy M
APPLICANT: Wells, Jeremy M
APPLICANT: Hanniffy, Sean B
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21122WO
CURRENT APPLICATION NUMBER: US/09/769,744A
CURRENT FILING DATE: 2001-01-26
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: GB 9816336.3
PRIOR APPLICATION NUMBER: GB 9816336.3
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: US 60/125329
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEO ID NOS: 196
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 23
LENGTH: 1455
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Matches 631;
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Publication No.
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ORGANISM: Streptococcus
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                                                       TGCTTCTGATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTA
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Pred. No. 1.5e-81;
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptcoccus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
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US-09-884-465A-1
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SEQ ID NO 1
LENGTH: 3120
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
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Best Local 9
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APPLICANT:
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                                                                                                                                                                                                             Local Similarity 65.3 hes 631; Conservative
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                    AATTACAGATCAGGGCTATGTAACGTCACACGGTGACCACTATCATTACTATAATGGGAA
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Martin, Denis
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Pred. No. 2.3e-81;
0; Mismatches 276;
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Sequence 2, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptcocccus Antigens
FILE REFERENCE: 055190-004
CURRENT FILLNG DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
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US-09-884-465A-2
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NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3
SEQ ID NO 2
LENGTH: 5048
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Pred. No. 2.9e-81;
0; Mismatches 276;
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Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
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Best Local Similarity 73.0%;
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APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptcocccus
FILE REFERENCE: 055190-0044
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                       TGCTTCTGATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTA
                                                           ---TGTTGCTGTAGCAAGGTCTCAGGGACGATATACGACAAATGATGGTTATGTCTTTAA
                                                                                           TGCTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTTTAA
                                                                                                                            CAATCGTCAAAAACAAGAACATGTCAAAGATAATGAGAAGGTTAACTCTAA------
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Martin, Denis
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Pred. No. 3e-72;
0; Mismatches 160;
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US-09-769-736-23
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CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: GB 9816335.5
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/125163
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver: 2.1
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LENGTH: 1146
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APPLICANT: Hanniffy, Sean B
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21089wo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Microbial Technics Limited APPLICANT: Le Page, Richard WF
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                                                                                                                                                                                                                                                                                                                         CACTTCACATGGCGACCACTATCATTACTACAATGGTAAGGTTCCTTATGACGCTATCAT
                                                  AACTAAAGAAGCTAAAGAAAAAGGTTTAGCTCAAGTGGCCCATCTCAGTAAAGAAGAAGT
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                                                                                 TAGTCAACATCGTGAAG-----
                                                                                                                AGGTAGTAAGCGCAAAAACATTCGAACCAAACAACAAATTGCTGAGCAAGTAGCCAAAGG
                                                                                                                                            TGAAATCTTAGACGGTTACGTTATTAAAGTCAATGGCAACTATTATGTTTACCTCAAGCC
                                                                                                                                                                                                       TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA
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Pred. No. 4.8e-40;
0; Mismatches 231;
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APPLICANT: Hamiffy, Sean B

TITLE OF INVENTION: Proteins
FILE REFERENCE: PMC/P21089wo
CURRENT APPLICATION NUMBER: US/09/769,736
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: GB 9816335.5
PRIOR APPLICATION NUMBER: US 60/125163
PRIOR PILING DATE: 1998-07-19
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US-09-769-736-17
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LENGTH: 24
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Best Local (
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      TAGTCAACATCGTGAAG--
                                                                                                                                                                                                                                           CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT
                                   AGGTAGTAAGCGCAAAAACATTCGAACCAAACAACAAATTGCTGAGCAAGTAGCCAAAGG
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Pred. No. 7.2e-40;
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      -- GTGGAACTCCAAGAAACGA 453
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TTACCATTACATTCCTAAGAATGAGTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTT
                                                                                                  TAGTCCGACAGATATCATTGATGATTTAGGAGATGCTTATTTAGTACCTCATGGTAATCA
                                                                                                                                                TAATGCTTCTGATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCA
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TTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTATAT 63 DB 12; 231; . Indels Length 2469; 30; Gaps

TAGTGAAGAGTTGTTGATGACGGATCCTAATTACCATTTTAAACAATCAGACGTTATCAA CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA 297 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAAATACTATGTTTACCTTAAGGA 357 TGAAATCTTAGACGGTTACGTTATTAAAGTCAATGGCAACTATTATGTTTACCTCAAGCC 425 305

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; LOCATION: Complement((4351)..(5214)) US-09-252-088-13
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            Query Match
Best Local Similarity
Matches 399; Conserv
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Publication No. US20030031682A1
GENERAL INFORMATION:
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APPLICANT: HAMEL, JOSE
APPLICANT: MARTIN, Denis
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 8331-9002
CURRENT APPLICATION NUMBER: US/09/252,088
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: US/60/075,425
EARLIER FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
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LOCATION:
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ORGANISM: group
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NAME/KEY: CDS
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             Score 209.8; DB 11; Length 5215; 
Pred. No. 2.6e-39; 
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US-09-884-465A-257
Sequence 257, Application US/09884465A
Publication No. US20030077293A1
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                                                                                          APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
                                                            SOFTWARE: PatentIn version 3.1 SEQ ID NO 257
                                                                                                                                                                                                                          APPLICANT:
          LENGTH: 819
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Sequence 71, Application US/09769736
Publication No. US20030138775A1
GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Le Page, Richard WF
APPLICANT: Wells, Jerremy M
APPLICANT: Hanniffy, Sean B
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21089wo
CURRENT APPLICATION UMBER: US/09/769,736
CURRENT FILING DATE: 2003-02-14
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Pred. No. 1.1e-37;
0; Mismatches 313;
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PRIOR FILING DATE: 1998-07-27
PRIOR PELICATION NUMBER: US 60
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 71
                                                                                                                                                                                                                                                                              RESULT 18
US-09-452-599-34/c
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                                                                                                                                                                                                                   Sequence 34, Application US/09452599 Patent No. US20020055101A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 306; Conserv
                                                        APPLICANT: Ouellette, Marc
APPLICANT: ROy, Paul H.
APPLICANT: ROY, Paul H.
INVENTION: Specific and Universal Probes and Amplification Primers
TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
FILE REFERENCE: 12287.31
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    CURRENT APPLICATION NUMBER: US/09/452,599
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 08/526,840
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FILING DATE: 1998-07-27
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Pred. No. 1.5e-17;
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LENGTH: 841
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
US-10-121-120-34
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US-10-121-120-34/c
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; ORGANISM: Streptococcus pneumoniae
US-09-452-599-34
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SOFTWARE: PatentIn Ve
SEQ ID NO 34
LENGTH: 841
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro FILE REFERENCE: 12287.31
CURRENT APPLICATION NUMBER: US/10/121,120
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 09/452,599
PRIOR APPLICATION NUMBER: 09/452,599
PRIOR FILING DATE: 1999-12-09
PRIOR PILING DATE: 1999-12-09
PRIOR PILING DATE: 1994-09-12
RIOR APPLICATION NUMBER: 08/304,732
PRIOR FILING DATE: 1994-09-12
NUMBER OF SEQ ID NOS: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Specific and Universal Probes and Amplification TITLE OF INVENTION: Primers
TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacteria
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PRIOR APPLICATION NUMBER: 08/2
PRIOR FILING DATE: 1994-09-12
PRIOR FILING DATE: 177
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2150 CCAGAAGTCCCTCAAGTAGAGACTGAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTT 2209
                                                                              2090 GAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAAACACCTGCTGAG 2149
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Conservative
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Pred. No. 1.1e-15;
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Pred. No. 1.1e-15;
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APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 08435/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: UP 2001/246789
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2179
LENGTH: 1168
RESULT 21
US-10-029-386-25433; A:
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; LOCATION: (201)..(968)
US-10-017-161-2179
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2179, Application US/10017161 Publication No. US20030143668A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                       CTTCTGATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCAT 574
                                                                                                                                                          ATCGACAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCCAAGAAACGATGGTG
                                                                                                                                                                                                                                                                                                ATGATGATGGTGGTGAGGACGATGGTGATGATGATGCTGGTGATGATGATGATA
                                                                                                                                                                                                                                                                                                                           ACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCA
                                                                                                                                                                                                                                                                                                                                                                   AAGATGAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAAAT 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTACGAAATAATTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAA 2329
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ilarity 48.3%;
Conservative
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Pred. No. 0.087;
0; Mismatches 153;
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Application US/10029386

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           FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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Matches
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CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 25433
LENGTH: 573
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                            Sequence 4012, Application Patent No. US20020048763A1
                                                                                                                                                                                                                                                APPLICANT: Penn,
APPLICANT: Rank,
APPLICANT: Hanze
APPLICANT: Chen,
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Best Local
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OTHER INFORMATION: MAP TO AL13323.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.16

OTHER INFORMATION: NT HIT: U63807.1, EVALUE 8.50e+00

-10-029-386-25433
                                                                                                                                                                                                        APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED
TITLE OF INVENTION: EXPRESSION ANALYSIS
FILE REFERENCE: AEOMICA-X-2
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162; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATAGTGATGATGATGATGGTGATGGCAATGATGATGATGGTGA
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                                                                                                                                                                                                                                                                                    Rank, David R.
DATE:
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Pred. No.
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Best Local Similarity
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OTHER INFORMATION: E
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OTHER INFORMATION: E:
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PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
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TYPE: DNA
ORGANISM: Homo sapiens
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APPLICATION NUMBER: US 09/608
FILING DATE: 2000-06-30
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R OF SEQ ID NOS: 49117
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FILING DATE: 2001-01-30
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                                   GGGATGATGACAGTGATGATGATGATGATGATGATGATGATGATGATGAT
                                                                       CTTCTGATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGAT 571
                                                                                                                                       CTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATG 518
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                                                                                                               GTGATGATGGGGGAAGATG---ATGACAGTGATGGTGGTGATGATGACGATAGCGATGATG
                                                                                                                                                                                                                              ATCGACAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTG 458
                                                                                                                                                                                                                                                                  ATGGTGATGATGGATGATGGTGATGATGATGATGACAGTGATGATGATGATGATGGTG 597
                                                                                                                                                                                                                                                                                                ACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCA 398
                                                                                                                                                                                           ATGATGGGGATGATGACAGTGATGATGGTGATGATGGTGATGGTGATGATGATGATA
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EXPRESSED IN BT474
EXPRESSED IN BRAIN
EXPRESSED IN HBLION
EXPRESSED IN HBLION
EXPRESSED IN HELA,
EXPRESSED IN ADULT
EXPRESSED IN FIACE
EXPRESSED IN FETAL
EXPRESSED IN HEART
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49.8; DB Pred. No. 0.25;
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IN BRAIN, SIGNAL = 2.1
IN LUNG, SIGNAL = 1.7
IN HEL100, SIGNAL = 2.3
IN HELA, SIGNAL = 2.7
IN PLACENTA, SIGNAL = 2.2
IN ADULT LIVER, SIGNAL = 2.2
IN FETAL LIVER, SIGNAL = 2.1
IN GETAL LIVER, SIGNAL = 2.1
IN BONE MARROW, SIGNAL = 2.3
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Length 1959; Indels

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Gaps

657

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Sequence 3, Application US/09901152
Publication No. US20030022824A1
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTIFILE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001248
CURRENT APPLICATION NUMBER: US/09/901,152
CURRENT APPLICATION NUMBER: US/09/901,152
CURRENT STILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 5
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US-09-901-152-3/c
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US-10-029-386-20619/c
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Best Local Similarity
Matches 148; Conserv
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: HANZEL, DAVID K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEOMICA-X-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Annomax Sequence Listing Engine vers. SEQ ID NO 20619
LENGTH: 506
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SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: FastSEQ for Windows Version 4.0 
EQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:

OTHER INFORMATION: MAP TO ACO02070.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.79

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No. 0.7;
0; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12;
                                                                                                             PROTEINS,
ENCODING HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                              SECRETED PROTEINS,
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RESULT 25
US-09-855-824-3/c
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                                                                                                                          Query Match 1.9%;
Best Local Similarity 46.4%;
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001233
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/855,824
                                                                                                                                                                                                   FEATURE:

NAME/KEY: misc_feature
LOCATION: (1)...(143601)

OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (1)...(58985)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                      ORGANISM: Human
                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                                                                                                                                                     ENGTH:
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GTGAAGACTTTGCCATCTG
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                                                                                                                         Score 45.4; DE Pred. No. 28; 0; Mismatches
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Pred. No. 17;
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                                                                                                                          171;
                                                                                                                                                       Length 143601;
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RESULT 26
US-09-864-761-18355
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
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APPLICANT:
                                                                                                                                                                                                                                                                                              PRIOR
SOFTWARE: Annomax Sequence
SEQ ID NO 18355
LENGTH: 423
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                                                           NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
                                                                       FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
                                                                                                                                                                                                              FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                                                                    APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                           APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00661
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Chen, Wensheng
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1, David K.
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                                    Listing
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PAPLICATION NUMBER: US 60/207,456
PRIOR PAPLICATION NUMBER: US 09/632,366
PRIOR PAPLICATION NUMBER: US 09/632,366
PRIOR PAPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR PAPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PAPLICATION NUMBER: PCT/US01/00667
PRIOR PAPLICATION NUMBER: PCT/US01/00667
PRIOR PAPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PRILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: Aeomica-X-1
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                                                       APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
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Chen, Wensheng
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EXPRESSED IN HELLA, SIG

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PCT/US01/00663
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D IN HELA, SIGNAL = 2.8

D IN BONE MARROW, SIGNAL = 1.4

D IN LUNG, SIGNAL = 1.4

D IN FETAL LIVER, SIGNAL = 1.9

D IN HEART, SIGNAL = 3.2

D IN BRAIN, SIGNAL = 3.2

D IN BRAIN, SIGNAL = 1.9

D IN BRAIN, SIGNAL = 2.2

D IN BRAIN, SIGNAL = 2.2
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Pred. No. 1
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FILING DATE:

2001-01-30

FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670 APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662

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RESULT 28
US-10-312-841-2
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-864-761-1597
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Best Local Similarity 51.8
Matches 101; Conservative
                                                                                                                                                                                                                                                   Sequence 2, Application US/10312841 Publication No. US20030186277A1 GENERAL INFORMATION:
                                                                                                    SEQ ID NO 2
LENGTH: 3673778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Annomax Sequence Listing Engine vers. SEQ ID NO 1597
                                                                                                                                 APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
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                                                            TYPE: DNA ORGANISM: Artificial Sequence
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OTHER INFORMATION:
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ORGANISM: Homo sapiens
                                  OTHER INFORMATION:
                                                   FEATURE:
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WAME/KEY: unsure
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FILING DATE: 2001-01-29
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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N: EXPRESSED IN HBL100, SIGNAL = 3.1

N: EXPRESSED IN HELA, SIGNAL = 2.8

N: EXPRESSED IN BONE MARROW, SIGNAL = 4.2

N: EXPRESSED IN FORTAL LIVER, SIGNAL = 2.6

N: EXPRESSED IN HEART, SIGNAL = 1.9

N: EXPRESSED IN BRAIN, SIGNAL = 3.2

N: EXPRESSED IN BRAIN, SIGNAL = 1.9

N: EXPRESSED IN BRAIN, SIGNAL = 1.9

N: EXPRESSED IN BRAIN, SIGNAL = 1.9

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
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                            chemically treated genomic DNA (Homo sapiens)
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Pred. No. 2.1;
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US-10-312-841-2
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                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
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Best Local Similarity
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROAPPAY
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
                                                  APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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                                  FILING DATE: 2001-01-30
                                                                                                        FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                  FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00667
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   NUMBER: PCT/US01/00670: 2001-01-30
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Pred. No. 2.1e+02;
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Best Local (
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              PRIOR PRIOR
                                          FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                       APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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             NT FILING DATE: 2001-05-23
APPLICATION NUMBER: US 60/180,312
FILING DATE: 2000-02-04
 APPLICATION NUMBER:
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N: EXPRESSED IN BY174, SIGNAL = 0.89

N: EXPRESSED IN HELLO, SIGNAL = 1.1

N: EXPRESSED IN HELLA, SIGNAL = 1.1

N: EXPRESSED IN HELLA, SIGNAL = 1

N: EXPRESSED IN HELLA, SIGNAL = 1

N: EXPRESSED IN HELLA, SIGNAL = 1.2

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2

N: SWISSPROT HIT: P17164, EVALUE 4.10e+00

CN: EST_HUMAN HIT: AW844901.1, EVALUE 2.90e+00
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Pred. No. 4.5;
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Best Local Similarity
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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APPLICATION NUMBER: US 09/608,408
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                                                                                                                 ACGCGGATAACGTCCGTACAAAAGAGAAAATCAATCGACAAAAACAAGAGCATAGTCAAC 425
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                                                                          ATGAAGATGACGATGATGAAGAGGAGGTTGGTGATGGTGATGATGGTGTTAATGGTGATG
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EXPRESSED IN BT474, SIGNAL = 1.1

EXPRESSED IN HACENTA, SIGNAL = 0.1

EXPRESSED IN HBL100, SIGNAL = 1.1

EXPRESSED IN HELA, SIGNAL = 1.8

EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
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Pred. No. 7.5;
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371
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FOR

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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN FAIN, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.6

OTHER INFORMATION: EXPRESSED IN HEART SIGNAL = 3.6

OTHER INFORMATION: EXPRESSED IN HEART SIGNAL = 3.6
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Best Local
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ORGANISM: Homo sapiens
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                                                                                                                                                                                          GATGATGACGATAGTGATGGTGGTGGTGGTGATGATGATGACGATAGTGATGGT
                                                                                                                                                                                                                                                                                                                                          GACGATGGTAATGGTGATAATGATGATGATGAAGAGGATGAAGATTATCACGATGGTAAT
  GATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCAT
                                                                                              GCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCT
                                                                                                                                                                                                                                              CAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTT
                                                                                                                                                                                                                                                                                                                                                                                             GGTGATGAGGATGGTGGTGAGGATGGTTACGATGGTGATGGTGGTGGTGACAGTGGA
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Pred. No. 5.2;
0; Mismatches
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                                                                                                                                                                 RESULT 33
US-09-864-761-19488
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                                                                                       Sequence 19488, Application Patent No. US20020048763A1 GENERAL INFORMATION:
                    APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K
APPLICANT:
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; OTHER INFORMATION: MAP TO AC007540.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.73
; OTHER INFORMATION: EST_HUMAN HIT: BE767903.1, EVALUE 1.00e-03
; OTHER INFORMATION: NT HIT: AJ252124.1, EVALUE 1.20e-02
US-10-029-386-22627
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US-10-029-386-22627/c
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LENGTH: 785
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Best Local Similarity
Matches 188; Conserv
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED
TITLE OF INVENTION: EXPRESSION ANALYSIS
FILE REFERENCE: AEOMICA-X-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 ATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTT
TGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATA
                                                                                                                                                                                                                                                          AACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCT
                                                                                                                                                                                                                                                                                                             TTGGTGATGATGGTGATGTCTGAGATGATGGTGGTGATGATAATGGTGATGGTGATG
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                                                  TCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCAT 580
                                                                                                     ATGATGGTGACGGTGATTATGATGGAGATGATGGTGATGGCGATAATGACGGAGATG
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CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 09/632,366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/236,359
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                                                           108
 168
                            338 TACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATC
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                                                           AAAGATGAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAA
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IN BOME MARROW, SIGNAL = 6
IN LUNG, SIGNAL = 2.9
IN BRAIN, SIGNAL = 6.5
IN ADULT LIVER, SIGNAL = 5
IN FETAL LIVER, SIGNAL = 1
IN PEACENTA, SIGNAL = 1.1
IN HEART, SIGNAL = 1.1
IN HELA, SIGNAL = 3.8
                                                                                                                               Score 42.4; DB 9;
Pred. No. 8.1;
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                                                                                                                   Mismatches 151;
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US-09-864-761-2772
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SOFTWARE: Annot
SEQ ID NO 2772
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60
PRIOR APPLICATION NUMBER: PCT/V
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/V
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/V
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                  PRIOR
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CURRENT FILING DATE: 2001-05-23
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                                                       LENGTH: 962
TYPE: DNA
ORGANISM: Homo sapiens
OTHER INFORMATION: MAP TO AC008125.9
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL
                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US (FILING DATE: 2000-06-30
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US20020048763A1
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David K.
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRIOR PRICING NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-2
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
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OTHER INFORMATION:
US-09-864-761-2772
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Best Local Similarity
                                                                          SEQ ID
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Patent No. US20020061569A1
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OTHER INFORMATION:
                                     NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4883
LENGTH: 4047
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           TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trawick, John D. Carr, Grant J.
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Conservative
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Pred. No. 9.9;
0; Mismatches 151;
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IN ADULT LIVER, SIGNAL = 5.8
IN FETAL LIVER, SIGNAL = 1.8
IN PLACENTA, SIGNAL = 5
IN HEART, SIGNAL = 1.1
IN HELA, SIGNAL = 3.8
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Query Match
Best Local Similarity
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US-09-815-242-9039
                                                                                                                                                                  PRIOR FILING DATE: 2001
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for W
SEQ ID NO 9039
LENGTH: 4050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Staphylococcus aureus US-09-815-242-4843
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26.
PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,
CURRENT FILLING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
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                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-11-27
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                                                                          NAME/KEY: CDS
LOCATION: (1)
                                                                                                               TYPE: DNA ORGANISM: Staphylococcus aureus FEATURE:
                                                                                                                                                                                                                                                                                                FILING DATE: 2000-12-
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/257,931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto, Robert T.
Xu, H. Howard
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Pred. No. 21;
0; Mismatches 146;
Score 42.4;
Pred. No. 21
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              Length 4050;
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US-08-781-986A-454/c
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                                                                                                                       US-08-781-986A-454
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                                                                                       Query Match
                                                            Matches
                                                                                                                                                                                                           FILLING FILLING ATTORNEY/AGENT IN.

NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248
TELECOMMUNICATION INFORMATION:
"FRLEPHONE: (301) 309-8512
(301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staph
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                  LENGTH: 4358 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS
SOFTWARE: ASCII Text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Rockville
STATE: Maryland
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                                                                          Local
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                            1695 AAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACCTCCATCTCCAGACG
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ATAAAGTTGAAGTTTCAACTGCCAAATCAGATGAGCAAGCTTCACCAAAATCTACGAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9410 Key West Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette, 3.50 inch, 1.4Mb
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                                                                          1.8%;
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                                                          ; Score 42.4; D; Pred. No. 22; 0; Mismatches
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RESULT 39
US-10-027-632-269927/c
US-10-027-632-269927, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-027-632-269927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ
SEQ ID NO 269927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/218,006
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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CURRENT FILING DATE: 2002-04-30
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Pred. No. 8.9;
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PRIOR FILING DATE: 1
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Best Local
                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                   PRIOR
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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                                                      FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
                                                                                                                  APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04
                                                                                                                                                APPLICATION NUMBER: US 09/632,366 FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                             No.
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FILING DATE: 1999-11-23
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                                                                                                    APPLICATION NUMBER: US 60/236,359
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                             FILING DATE
                                          APPLICATION NUMBER: PCT/US01/00667
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                                                                                                                                                                                                                                                                                                                                                                                           19262, Application US/09864761 o. US20020048763A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAAGAAGAAGAAG 252
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Chen, Wensheng
DATE
                                                                                                                                                                                                                                                                                                                                                 Rank,
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               NUMBER: PCT/US01/0066
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                             2001-01-30
                                                                                                                                                                                                                                                                                                                                David K.
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SEQ ID NO 19262
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                             Sequence 2534, Application Patent No. US20020048763A1
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/864,761
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APPLICATION NUMBER: US 09/774,203
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APPLICATION NUMBER:
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NN: EXPRESSED IN HBL100, SIGNAL = 1.8

NN: EXPRESSED IN HEART, SIGNAL = 3.9

NN: EXPRESSED IN BONE MARROW, SIGNAL = 2.7

NN: EXPRESSED IN HELA, SIGNAL = 2.4

NN: EXPRESSED IN HEAL, SIGNAL = 2.8

NN: EXPRESSED IN LUNG, SIGNAL = 2.8

NN: EXPRESSED IN BT474, SIGNAL = 3.6

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
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NT HIT: U67539.1,
EST_HUMAN HIT: BF1
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN HEALTO, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN HEARI, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN HEARIN, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.6
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APPLICATION NUMBER: US 09/774,203
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APPLICATION NUMBER: US 60/207,456
FILING DATE: 2000-05-26
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                                    2158 CCCTCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAG
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ANATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGT 2157
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US-10-017-161-1913
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SEQ ID NO 1913
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CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
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TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED
FILE REFERENCE: 084335/0152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSI
APPLICANT: AKIYAMA, YU
APPLICANT: ABURATANI, I
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LOCATION: (26)
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LOCATION: (201)..(437)
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Local Similarity 45.8%;
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TGATAGTGATAACGGTGATGATGGTGGTGATGATAATGGTGA 3052
                                   CGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597
                                                                                                     AGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATACTGGTGATGCTTATAT 555
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                                                                                                                                                                                         TGGAACTCCAAGAAACGATGGTGCTTGCCTTGGCACGTTCGCAAGGACGCTATACTAC 495
                                                                                                                                                                                                                                                                                                                                          TATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGT 378
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                                                                         TGGTAATGGTAATCATGGTGATGATGGTGGTGATAGTAATCATGGTGACGGTAATGA 2950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB Pred. No. 25; 0; Mismatches
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                                                                             3010
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RESULT 43 US-10-029-386-5350/c

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.

Sequence 5350, Application US/10029386 Publication No. US20030194704A1

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RESULT 44
US-10-029-386-24901/c
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                                                                                                                                                                                                       Sequence 24901, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 5350
LENGTH: 528
                                      APPLICANT: RAIK, DAVIG R.

APPLICANT: HAIZEL, DAVIG R.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEGOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE. ABSOLUTE SECONDARY SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity Matches 176; Conserv
     SEQ ID
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Best Local
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: AEOMICA-X-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
                                SOFTWARE:
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OTHER INFORMATION: WAP TO AL049773.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.6

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6.8

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.4

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.2

OTHER INFORMATION: EXPRESSED IN BG654582.1, EVALUE 3.00e-12

OTHER INFORMATION: NT HIT: AL163283.2, EVALUE 6.00e-10
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               436
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                           Annomax Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGTACAAAAGAGGAAATCAATCGACA---AAAACAAGAGCATAGTCAACATCGTGAAGG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGACGGTGATTATAGTGATAATGATGGTGATCATGGTGATGATGGTGCTGCTGCTGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGATGGTGATGGTGGTGGTGGTGACAGTGATAAAGGTGATGGTGATGGTAATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATACTGGTGATGCTTATAT 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGTAATGGTAATCATGGTGATGATGGTGGTGGTGATAGTAATCATGGTGACGGTAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTAC 495
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Pred. No. 10;
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                           Engine
                              vers.
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US-10-312-841-1/c
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                                                                                                                                                                                                                                                                                                                  US-10-312-841-1
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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden
FILE REFERENCE: E01/1208/WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10312841 Publication No. US20030186277A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 157; Conserv
                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: unsure
NAME/KEY: (3294164)
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                                                                                                                                                                                                               Matches
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CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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  2061095
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                                                   737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 TATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAAT
                                                                                                                                                                                                             l Similarity
67; Conserv
                                   ACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCAAGCAA
                                                                                                                                                      CGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTCTGTAAGCAATCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGACAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCT
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EXPARSED IN HELA, SIGNAL = 0.46

SWISSPROT HIT: Q28084, EVALUE 6.50e+00

NT HIT: U13008.1, EVALUE 3.90e+00

EST_HUMAN HIT: BE409401.1, EVALUE 5.70e+00
                                                                                                                                                                                                                                                                                                                                                                                                                 chemically treated genomic DNA
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61.5%;
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                                                                                                                                                                                                          Score 41.8; DB 12;
Pred. No. 6.3e+02;
0; Mismatches 42;
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Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                    (Homo sapiens)
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                                                                                                                                                                                                                                                           Length 3673778;
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OTHER INFORMATION: MAP TO AL138895.4

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6

OTHER INFORMATION: NT HIT: AJ223271.1, EVALUE 3.90e-01

OTHER INFORMATION: SWISSPROT HIT: Q44052, EVALUE 2.00e+00

OTHER INFORMATION: EST_HUMAN HIT: BG981138.1, EVALUE 1.00e-130
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US-10-029-386-14986/c
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 47
                                                                                                                                                                                                                                                                                                        Sequence 1284, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
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                                                                                  SEQ ID NO 1284
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOMICA-X-2
                                                                                                                                                                               APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
                                                                                                                    CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Annomax Sequence Listing Engine vers. SEQ ID NO 14986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 34288
                                                                                                   SOFTWARE: Annomax Sequence
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
    FEATURE:
                   ORGANISM: Homo sapiens
                                        TYPE: DNA
                                                           ENGTH: 571
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                                                                                                   Engine vers.
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Best Local
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Best Local
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LOCATION: (1)...(611)
OTHER INFORMATION: n =
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OTHER
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ORGANISM: Homo sapiens
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2140 ACCTGCTGAGCCAGAAGTCCCCTCAAGTAGAGACTGAAAAAGTAGAAGCCCCAACTCCAAAGA 2199
                                                                                                 2080 AGACCACAGTGAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAAC 2139
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                                                               AGAAAAGAAAGCAAAAGCAGAAGCTAAACGGAAGGAGCAAGAAGCTAAAGAAAAACAAAG 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secrist,
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SOFTWARE: Corixa Invention Disclosure Database SEQ ID NO 233
LENGTH: 611
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APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.523
CURRENT APPLICATION NUMBER: US/09/864,864
CURRENT FILING DATE: 2001-05-23
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NN: EXPRESSED IN LUNG, SIGNAL = 1.7

NN: EXPRESSED IN HELA, SIGNAL = 2.1

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7

NN: EXPRESSED IN HEART, SIGNAL = 1.5

NN: EXPRESSED IN HEART, SIGNAL = 4.1

NN: EXPRESSED IN PLACENTA, SIGNAL = 1.6

NN: EXPRESSED IN PLACENTA, SIGNAL = 1.6
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Score 41.6; DE Pred. No. 12; 0; Mismatches
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Pred. No. 12;
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Sequence 50, Application US/09919497

Patent No. US2002010662A1

GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENIFILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
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US-09-864-864-313
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US-09-919-497-50
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Best Local Similarity
Matches 95; Conserv
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SEQ ID NO 313
LENGTH: 1845
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/864,864
CURRENT FILING DATE: 2001-05-23
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.523
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Benson, Darin R.
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Lodes, Michael J.
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Nucleic acid pneumoniae - protective or
The present sequence represents a protein from Streptococcus pneumoniae. The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or
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detection; pne
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               standard;
                                                                                     LLKGSNPSSVSKEKIN
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                                                                                                                                                                                                                               NRVKGEKRI PLVRLPYMVEHTVEVKNGNLI I PHKDHYHNI KFAWFDDHTYKAPNGYTLED
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                                                                        LLKGSNPSSVSKEKIN
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                                                                                                                                                                     LFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVP
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Pred. No. 3.5e-299;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choi
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                           polynucleotides encoding the S. pneumoniae antigens can be used to detect Streptococcus nucleic acids. ABQ84905 to ABQ85130 represent primers used in the cloning of S. pneumoniae ORFs (open reading frawhich are used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                       Chaim 11;
                                                                                                                                                                                                                                                                                                                                                                                          New Streptococcus pneumoniae antigens, useful for detecting Streptococcus and for preventing or attenuating disease caustreptococcus infection.
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                                            GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
                                                                                    AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT
                                                                                                                SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA
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                               GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
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; Streptococcal infection; det;
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Pred. No. 3.5e-299;
Mismatches 0;
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New proteins and nucleic acid molecules from Streptococcus useful as medicaments for treating or preventing a disease
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                                                                                       N-PSDB;
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pneumoniae, or infection

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Streptococcus pneumoniae type 4 strain genomic sequence appearing as CC ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or CC antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides CC which are the nucleic acid cited above or fragments between nucleotides CC ended to the sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers complement of the target sequence, and where the parts of the primers complement to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae batterium, where one or more CC genes encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain processing regions from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic sequence.
Note: The sequence data for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
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VSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTN
                                                                                 PQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQES
                                                                                                                                                               ARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPG
                                                                                                                                                                                                                                                                                      GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
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                  LLKGSNPSSVSKEKIN 796
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                                                                     QVETEKVEAQIKEAEVILLAKVTDSSLKANATETLAGIRNNLTLQIMDNNSIMAEAEKLLA
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Streptocourage residue, histidine triad residue, histidine triad residue, and history residue residue.
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                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant variant of Sp36 (Sp36A) of S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-2000
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                                                                                                                                                                                                                                                                                                                             lobar pneumonia
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                                                                                                                                                                                                                                                                                                                                              pneumoniae; infection; vaccine; coiled coil region;
ad residue; Sp36; antibody; otitis media;
l infection; bronchial infection; bronchitis; sepsis
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                                   /label= Coiled coil region
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                                                                                                                                           Query Match
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Matches 616
                                                                                                                                                                                                                                                                          antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the protein they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents the S. pneumoniae BVH-11M protein antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; prophylaxis; therapy; infection; diagnosis; menir otitis media; pneumonia; immunisation; bactericic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptcoccus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptcoccal infections in mammals (especially humans) which result in, e.g. meningitis, ortis media, bacteraemia and/or pneumonia. The present sequence represents a s. pneumoniae BVH-11 protein antigen, from the present invention.
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                                                                                                                                                           The invention describes an isolated polypeptide (I) with 70-90% CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II) CC comprising (I) is useful for therapeutic or prophylactic treatment of CC meningitis, otitis media, bacteraemia or pneumonia infection in an CC individual susceptible to these disorders. (II) is also useful for CC therapeutic or prophylactic treatment of any streptococcus bacterial CC infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus pneumoniae, group B Streptococcus such as Streptococcus pneumoniae, S. objection. CC Staphylococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia or CC Staphylococcus aureus) in an individual susceptible to the infection. CC Staphylococcus aureus) in an individual susceptible to the infection. CC test for S. pneumoniae infection. (III) is useful in DNA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probase for use in detecting the presence of Streptococcus in a biological content of the content of the presence of Streptococcus in a biological content of the content of the presence of Streptococcus in a biological content of the content of the presence of Streptococcus in a biological content of the content of the
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                                                              probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a truncate of a Streptococcus pneumoniae gene used to obtain antigenic peptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine component or preventing streptococcal infections such as otitis med
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described in the method of the invention.

Note: This sequence does not appear in the specification been created according to information given in the invent
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(first entry)

Streptococcus pneumoniae BVH-11 protein antigen SEQ ID

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; prophylaxis; therapy; infection; diagnosis; meningitis; be otitis media; pneumonia; immunisation; bactericidal.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Pred. No. 3.6e-229;
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           The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, oticis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus pneumoniae, group A
                                                                                                                                                   New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components f or preventing streptococcal infections such as otitis media, meningitis, and bacteraemia -
                                                                                                                                                                                                                    N-PSDB;
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                            KANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGS
                                                                                       EETPREEKPQSEKPESPKPTEEPEEESSEESEEPQVETEKVEEKLREAEDLLGKIQDPII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae.
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otitis media; pneumon:
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                                                                                                                                                                                                                                                                 SHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVNGKYYVYLKDA
                                                                                                                                                                                                                                                                                             SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 690 AA;
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The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants BVH-3 or BVH-11 or chimeric sequences derived from them. A vaccine comprising (I) is useful for therapeutic or prophylactic treatment omeningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus pneumoniae, group A
                                                                                                                                                                                                                                                                            New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components or preventing streptococcal infections such as otitis medimeningitis, and bacteraemia
                                                                                                                                                                                                                             Example 1; Page -; 113pp; English.
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RESULT 12 AAY91939 ID AAY91

AAY91939

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Matches 556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA
              TLEDLFATIKYYVEHPDERPHSNDGWGNA
                                                                            AAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGY
                                                                                                                                                                                                    ESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHD
                                                                                                                                                                                                                                                               KQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVNGKYYVYLKDA
TLEDLLATVKYYVEHPNERPHSDNGFGNA
                                                         EATYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLTTPHYDHYHNTKFEWFDEGLYEAPKGY
                                                                                                                      IISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSA
                                                                                                                                                                                    VSSDKVKLVDDILAFLAPIRHPERLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRD
                                                                                                                                                                                                                                                                                                           POPAPNPOPAPSNPIDEKLVKEAVRKVGDGYVFEENGVSRYIPAKNLSAETAAGIDSKLA
                                                                                                                                                                                                                                                                                                                            PQPAPNLK-IDSN---SSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLS
                                                                                                                                                                                                                                                                                                                                                                      ARGVAVPHGNHYHFIPYEQMSELEKRIARIIPLRYRSNHWVPDSRPEEPSPQPTPEPSPS
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Pred.
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No. 2.9e-210;
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690
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Matches 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptide is used to stimulate immune system and immunize treat a mammalian subject against Streptococcus pneumoniae infection colonization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human C3-degrading protein; 92 kDa; immunostimulatory; vaccine; inhibitor; inflammation; organ rejection; xenotransplantation.
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                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Page 55-57; 63pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-283594/24.
N-PSDB; AAA08557.
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31-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pneumoniae 92 kDa human C3-degrading protein
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AMERICAN CYANAMID
                  SVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSR
                                                                         TGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVP
                                                                                                                              AAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIED
                                                                                                                                                                                        TSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKD
                                                                                                                                                                                                                                                   SYELGLYQARTV-KENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYV
NPAQPRLSENHNLTVTPTYHQ-NQGENISSLLRELYAKPLSERHVESDGLIFDPAQITSR
                                                                                                               AAHADNIRTKEEIKROKOEHSHNHGGGS--NDOAVVAARAOGRYTTDDGYIFNASDIIED
                                                                                                                                                                      TSHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVDGKYYVYLKD
                                                                                                                                                                                                                               SYELGRHQAGQVKKESNRVSYIDGDQAGQKAENLTPDEVSKREGINAEQIVIKITDQGYV
                                                       TGDAYIVPHGDHYHYIPKNELSASELAAAEAYWNG
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                                                                                                                                                                                                                                                                                                                                                  826 AA;
                                                                                                                                                                                                                                                                                          Conservative
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99US-0283094.
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Pred. No. 4.1e-199;
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RESULT 13
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New proteins and nucleic acid molecules from Streptococcus useful as medicaments for treating or preventing a disease due to streptococcus bacteria, such as pneumonia, sepsis, o
                                                                                                                                                                                                                                                                    Bacterial meningitis; pneumonia; sepsis; otitis ear infection; antiinflammatory; antibacterial; auditory; respiratory; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                        S. pneumoniae
                                                   WPI; 2003-040579/03
N-PSDB; ABX06885.
                                                                                                                                                                                                                                                Streptococcus pneumoniae type 4 strain
                                                                                                                                                                                                                                                                                                                                                                                                 ABU01597 standard;
                                                                                     Masignani V,
                                                                                                                                                27-MAR-2001; 2001GB-0007658
                                                                                                                                                                        27-MAR-2002; 2002WO-IB02163
                                                                                                                                                                                                                         WO200277021-A2
                                                                                                                                                                                                                                                                                                                                                                          ABU01597;
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                                                                                                                         (CHIR-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as CC ABS5454. Also included are an antibody which binds one of the CC proteins, treating a patient by administering first and second primers, antibody (in a composition), a kit comprising first and second primers. CC which are the nucleic acid cited above or fragments between nucleotides CC which are the nucleic acid cited above or fragments between nucleotides CC where the first primer is substantially complementary to the target sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target CC sequence and the second primer is substantially complementary to the complementary substantial complementary to the target CC sequence to be amplified, assay comprising contacting a test compound CC with the protein, and determining whether the test compound binds to the CC genes encoding the proteins has been rendered inactive. The proteins, complementary to treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, cepsies, diagnostics and antibiotics. The methods are useful for compound compositions are useful for compositions are discussed by the identified coding regions from the CC denomic sequence.
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                                  SVSHTLTAKKENVAPROQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDEST
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4; Mismatches 138; Indels 47;
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AAY81501 to AAY81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be useful for the detection and diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are alsuseful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the
                                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing or inhibiting expression of the protein -
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                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 99-100; 108pp; English.
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                                  Protein;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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NPAQPRLSENHULTVTPTYHQ-NQGENISSLLRELYAKPLSERHVESDGLIFDPAQITSR
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                                                                                                                    Brodeur BR,
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                                                  antigens useful for vaccinating bacteremia and/or pneumonia -
                                                                                                                                                                                                                                                                                pneumoniae
                                                                                                                                                                                                                                                                                                                    pneumoniae; BVH-3; BVH-11; BVH-28; antigen; therapy; infection; diagnosis; meningitis; ba
                                                                                                                                                                                                                                                                                                       pneumonia; immunisation; bactericidal
                                                                                                                                                                                                                                                                                                                                                            pneumoniae strain
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                                                        LKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGS 785
                                                                                                                                                            DLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEE------PVEET
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                                          IKSNAKETLTGLKNNLLFGTQDNNTIMAEAEKLLALLKES
                                                                                                                                               DLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKPNEEKPQTEKPEEET
                                                                                                                                                                                                   YNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGYSLE
                                                                                                                                                                                                                     YNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLE
                                                                                                                                                                                                                                                    DEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAI
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                                                                                            PREEKPOSEKPESPKPTEEPEEESPEESPEESEEPOVETEKVKEKLREAEDLLGKIONPI
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Pred. No. 3.3e-197;
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                                                                                                            - PAEPEVPQVETEKVEAQLKEAEVLLAKVTDSS
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                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcal otitis media,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae; BVH-3; EVH-11; BVH-28; antiger prophylaxis; therapy; infection; diagnosis; meningitis; otitis media; pneumonia; immunisation; bactericidal.
                                                                                                                                                                                                                                                                                 Sequence
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          TARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSP
                                    NPAQPRLSENHULTVTPTYHQ-NQGENISSLLRELYAKPLSERHVESDGLIFDPAQITSR
                                                                                                                   AAHADNIRTKEEIKROKQEHSHNHGGGS--NDQAVVAARAQGRYTTDDGYIFNASDIIED
                                                                                                                                  AAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIED
                                                                                                                                                          TSHGDHYHYYNGKVFYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVDGKYYVYLKD
                                                                                                                                                                      TSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKD
                                                                                                                                                                                                SYELGRHQAGQVKKESNRVSYIDGDQAGQKAENLTPDEVSKREGINAEQIVIKITDQGYV
                                                SVSNPGTININTSNNSNINSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSR
                                                                                          TGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVP
TARGVAVPHGNHYHFIPYEQMSELEKRIARIIPLRYRSNHWVPDSRPEQPSPQSTPEPSP
                                                                             TGDAYIVPHGDHYHYIPKNELSASELAAAEAYWNG------KQGSRPSSSSSYNA
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Pred. No. 3.7e-196;
1; Mismatches 144;
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RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                                        histidine triad residue; Sp36; antibody; otitis media; nasopharyngeal infection; bronchial infection; bronchimeningitis; lobar pneumonia.
                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB01466;
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21-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Although
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AAAI YNR VKGEKRI PLVRLPYMVEHTVEVKNGNLI I PHKDHYHNI KFAWFDDHTYKAPNG
                                                                                DIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDS
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                                                  DITSDEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  838 AA;
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Pred. No. 3.9e-196;
1; Mismatches 144;
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         The invention relates to a protein comprising or having at least 50% CC identity to any of the 2469 amino acid sequences, identified in the CC specification (available on a computer readable format), or its fragment, CC expressed from 2469 of 2489 identified DNA coding regions from the CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as CC ABS56454. Also included are an antibody which binds one of the CC proteins, treating a patient by administering the protein, DNA or CC which are the nucleic acid cited above or fragments between nucleotides CC which are the nucleic acid cited above or fragments between nucleotides CC which are the sequence not defined in the specification, for amplifying a CC target sequence contained within a Streptococcus nucleot acid sequence, CC where the first primer is substantially complementary to the target CC complement of the target squence, and where the parts of the primers CC sequence and the second primer is substantially complementary to the target CC sequence to be amplified, assay comprising contacting a test compound CC with the protein, and determining whether the termining to the target contained in and a Strantococcus and above the test compound brinds to the protein, and strantococcus and above the termining to the target contains and a Strantococcus and above the termining to the target contains and strantococcus and above the termining to the target contains and strantococcus and above the termining to the target contains and strantococcus and above the termining to the termining to the target contains and active the termining to the target contains and a strantococcus and above the termining to the target contains and active the termining to the target contains and active the termining to the target contains and active the termining to the target contains and the second brinds to the contains and the termining the termining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or ear infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-2001; 2001GB-0007658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacterial meningitis;

    pneumoniae type 4 strain protein from coding region #993.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1986; 56pp;
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pneumoniae bacterium,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the printed specification, format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic sequence.

Note: The sequence data for this patent did not form part

Note the printed specification, but was obtained in electronic
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                                                                                                                YTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGK------KDHSE------
                                                                                                                                                                             AAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNG
                                                                                                                                                                                                                                         DIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDS
                                                                                                                                                                                                                                                                                   DVPSDKVKLVDDILAFLAPIRHPERLGKENAQITYTDDEIQVAKLAGKYTTEDGYIFDPR
                                                                                                                                                                                                                                                                                                    DESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEH
                                                                                                                                                                                                                                                                                                                                                                                                               SPQPAPNPQPAPSNPIDEKLVKEAVRKVGDGYVFEENGVSRYIPAKDLSAETAAGIDSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                               GPOPAPNIK-IDSN---SSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKL
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                                                                                                                                                         AEAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKG
                                                                                                                                                                                                                      DITSDEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKG
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AKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSV 790
                             ESDEKENHAGINPSADNLYKPSTDTEETEEEAEDTTDEAEIPQVENSVINAKIADAEALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TARGVAVPHGNHYHFIPYEQMSELEKRIARIIPLRYRSNHWVPDSRPEQPSPQSTPEPSP
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                                                                                          YTLEDLLATVKYYVEHPNERPHSDNGFGNASDHVRKNKVDQDSKPDEDKEHDEVSEPTHP
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                                                           -DPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKEAEVLL
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptcoccus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptcoccal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents a s. pneumoniae BVH-11 protein antigen, from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcal otitis media,
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TGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVP
                                                                                                                                                            AAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIED
                                                                                                                                        AAHADNIRTKEEIKROKOERSHNHNS---RADNAVAAARAOGRYTTDDGYIFNASDIIED
                                                                                                                                                                                                                     TSHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVDGKYYVYLKD
                                                                                                                                                                                                                                                         TSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        807 AA;
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                                                                                                                                                                                                                                                                                                                                                                                             Score 2771; DB 21;
Pred. No. 4.3e-196;
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diagnosis; meningitis; bacteraemia;
ation; bactericidal.
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                                                                                                                                                                                                                                                    Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal.
 Disclosure; Fig 12; 106pp; English
                       Streptococcal otitis media,
                                                                                                                                 23-DEC-1998;
                                                                                                                                                         20-DEC-1999;
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Best Local Similarity
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                                 TDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGS
                                                                                                                                                                                                                     DIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDS
                                                                                                                                                                                                                                                      TGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVP
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                                                                                                                          YTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEE-----P
                                                                                                                                                                     AAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNG
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             QNPIIKSNAKETLTGLKNNLLFGTQDNNTIMAEAEKLLALLKES
                                                                                                                                                         AEATYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKG
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                                                                                                            YSLEDILLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKPNEEKPQTEKP
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Pred. No. 2
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ed. No. 2.8e-195;
Mismatches 141;
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Best Local Similarity
Matches 538; Conserv
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                                                                                                                                                                                                                                                                                                                                                         Sequence
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TARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPS-
                                                    SVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSR
                                                                           TGDAYIVPHGDHYHYIPKNELSASELAAAEAYWNG-----KQGSRPSSSSSYNA
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                         NPVQPRLSENHNLTVTPTYHQ-NQGENISSLLRELYAKPLSERHVESDGLIFDPAQITSR
                                                                                                                                     AAHADNIRTKEEIKROKQEHSHNHNS---RADNAVAAARAQGRYTTDDGYIFNASDIIED
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Pred. No. 1.5e-194;
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                                Disclosure; Fig 12; 106pp; English
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                                                                                                                 Hamel J,
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                                                                                                                                                                                                                                                                                  pneumonia; immunisation;
                                                                                                                                                                                                                                                                                                                                pneumoniae strain SP64 BVH-11-2
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The present invention describes nucleic acid antigens (II) from Streptococcus pneumoniae.

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encoding protein protein antigens

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                                                                                                                                                                                                       NGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGK-----
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LLEKVTDPSIRQNAMETLTGLKSSLLLGTKDNNTISAEVDSLLALLKESQPAPI 818
                                         LLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSV
                                                                                       HPESDEKENHAGLNPSADNLYKPSTDTEETEEEAEDTTDEAEIPQVENSVINAKIADAEA
                                                                                                                                                                           KGYSLEDLLATVKYYVEHPNERPHSDNGFGNASDHVRKNKADQDSKPDEDKEHDEVSEPT
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Pred.
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No. 1.5e-194;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                              infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus progenes, group B Streptococcus such as Streptococcus progenes, group B Streptococcus such as Streptococcus galactiae, S. dysgalactiae, S. uberis, S. nocardia or Staphylococcus aureus) in an individual susceptible to the infection. A streptococcus polynucleotide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a truncate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants BVH-3 or BVH-10, or chimeric sequences derived from them. A vaccine comprising (I) is useful for therapeutic or prophylactic treatment compnigitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapeutic or prophylactic treatment of any streptococcal bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media, meningitis, and bacteraemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia; pneumonia; streptococcal bacterial infection; mutant; mutein.
                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                       Note: This sequence does not appear in the specification but has been created according to information given in the invention.
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                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae gene used to obtain antigenic peptides, ribed in the method of the invention.
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                                                                                              SYELGLYQARTV-KENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYV
 TSHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVDGKYYVYLKD
                     TSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKD 119
                                                                        SYELGRHQAGQVKKESNRVSYIDGDQAGQKAENLTPDEVSKREGINAEQIVIKITDQGYV
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                                                                                                                                               Score 2750.5; DB 23;
Pred. No. 1.5e-194;
90; Mismatches 145; ]
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                                                                                                                                                                                                                                                                                               standard;
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                                                                                                                                       pneumoniae
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             PHARMA INC
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KGYSLEDLLATVKYYVEHPNERPHSDNGFGNASDHVRKNKADQDSKPDEDKEHDEVSEPT
                 NGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGK------
                                              PRDITSDEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEA
                                                                                                                 EHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTG
                                                                                                                                                                   LNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFD
                                                                                                                                                                                                      KLAKQESLSHKLGAKKTDLPSSDREFYNKAYDLLARIHQDLLDNKGRQVDFEVLDNLLER
                                                                                                                                                                                                                KLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLER
                                                                                                                                                                                                                                                       SLQPAPNPQPAPSNPID--EKLVKEAVRKVGDGYVFEENGVSRYIPAKDLSAETAAGIDS
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The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the protein they encode. The protein antigens may then be used as vaccines for t prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents the S. pneumoniae BVH-11-2 protein antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcal antigens useful for vaccinal otitis media, bacteremia and/or pneumonia
Score 2750.5; DB 2. Pred. No. 1.5e-194; 0; Mismatches 145;
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                                                                                                                                                                                 CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II) CC comprising (I) is useful for therapeutic or prophylactic treatment of CC meningitis, otitis media, bacteraemia or pneumonia infection in an CC individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcus useful for CC infection (e.g., caused by Streptococcus pneumoniae, group A CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such as Streptococcus pyogenes, group B Streptococcus such as Streptococcus pyogenes, S. uberis, S. nocardia or CC staphylococcus aureus) in an individual susceptible to the infection. CC A polymucleotide (III) encoding (I) is useful in DNA immunisation CC techniques. The Streptococcus polypetides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA CC probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be CC used for detecting circulating S. pneumonia nucleic acid in a sample for CC Streptococcus pneumoniae protein BVH-11-2, used to create the antigenic peptides described in the method of the invention.
   Query Match
Best Local Similarity
Matches 538; Conserv
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                                                                                                                               Sequence
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                            pneumonia; immunisation; bactericidal
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therapy; infection; diagnosis; meningitis; bacteraemi
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Matches 538
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                                                                                               SKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTBAHKALFXNKGRNSDFQALDKLLERLN
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                                                   DESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEH
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                The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents a S. pneumoniae BVH-11-2 protein antigen, from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; prophylaxis; therapy; infection; diagnosis; meningitis; bootitis media; pneumonia; immunisation; bactericidal.
Sequence
                                                                                                                                             Disclosure; Fig 12; 106pp; English
                                                                                                                                                                                   Streptococcal
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Query Match Best Local Similarity

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Score Pred.

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           Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcal antigens useful for vaccinating otitis media, bacteremia and/or pneumonia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                          TSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYYYLKD 119
                                                                      QESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDE 477
                                                                                                           APNPOPAPSNPID--EKLVKEAVRKVGDGYVFEENGVSRYIPAKDLSAETAAGIDSKLAK
                                                                                                                           TARGVĀVÞHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVÞDSRÞEQÞSÞQ--PTÞEÞ
                                                                                                                                                                                                                                                                         TGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVP
                                                                                                                                                                                                                                                                                                             AAHADNIRTKEEIKROROEHSHNHGGGS--NDQAVVAARAOGRYTTDDGYIFNASDIIED
                                                                                                                                                                                                                                                                                                                           AAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIED
                                                                                                                                                            TARGVAVPHGNHYHFIPYEQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPSPSPQP
                                                                                                                                                                                                                                                             TGDAYIVPHGNHFHYIPKSDLSASELAAAQAYWNG------KQGSRPSSSSSHNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2727; DB 21;
Pred. No. 7.9e-193;
)1; Mismatches 144;
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                                                                                  The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents a s. pneumoniae BVH-11 protein antigen, from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antiger prophylaxis; therapy; infection; diagnosis; meningitis; otitis media; pneumonia; immunisation; bactericidal.
                                                                                                                                                                                                                 Streptococcal antigens useful for vaccinating otitis media, bacteremia and/or pneumonia -
                                                                                                                                                                                                                                                                       Hamel J,
                                                                Sequence
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  SYELGLYQA-RTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYV
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                       98;
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                     Score 2720; DB 21;
Pred. No. 2.6e-192;
8; Mismatches 142;
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658 LEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 NPAQPRLSENHNLTVTPTYHQ-NQGENISSLLRELYAKPLSERHVESDGLIFDPAQITSR
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                                  VTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGS
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AAB12762;
AAB12762;
AAB12762;
21-NOV-2000 (first entry)
Streptococcus pneumoniae strain A66 BVH-11 protein antigen.
Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal.
Streptococcus pneumoniae.
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TSDEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAE
                     ISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAA
                                                  QESLSHKLGTKKTDLPSSDREFYNKAYDLLARIHQDLLDNKGRQVDFEALDNLLERLKDV
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Pred. No. 2.6e-192;
8; Mismatches 142;
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or pneumonia -
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Gaps

SYELGRHQAGQDKKESNRVAYIDGDQAGQKAENLTPDEVSKREGINAEQIVIKITDQGYV

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RESULT 32
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                                                                             have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the protein they encode. The protein antigens may then be used as vaccines for t prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents as s, pneumoniae BVH-11-2 protein antigen, from the present invention.
                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus
                                                                                                                                                               The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens
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otitis media; pneumonia;
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therapy; infection; diagnosis; meningitis; bacteraemia;
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        Score 2714; DB 21;
Pred. No. 7.3e-192;
0; Mismatches 146;
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therapy; infection; diagnosis; meningitis; bacteraemi
pneumonia; immunisation; bactericidal.
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Matches 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcal otitis media,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 12; 106pp; English
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                                                               ISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAA
                                                                                                       SSDKVKLVEDILAFLAPIRHPERLGKPNSQITYTDDEIQVAKLAGKYTTEDGYIFDPRDI
                                                                                                                       STNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDI
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8; Mismatches 143;
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        The present sequence represents a protein from Streptococcus pneumoniae. The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to
                                                                                                                                           Claim
                                                                                                                                                               Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
                                                                                                                                                                                                                                                                                                31-OCT-1996;
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tis media; meningitis
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passive
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RESULT 35
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AC ABP54
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ABP54589

standard;

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(first entry) SP042

pneumoniae

protein

sequence

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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.
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                                                                                                                                      AAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNG 655
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                               VEET--
                                                                         YTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEE-----P 709
                                                                                                                                                                                                                                                DVXSDKVKLVXDILAFLAPIRHPERLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPR
                                                                                                                                                                                                                                                                                                           AKQESLSHKLGAKKTDLPSSDREFYNKAYDLLARIHQDLLDNKGRQVDFEALDNLLERLK
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EEETPREEKPQSEKPESPKPTEEPEESPEESEEPQVETEKVEEKLREAEDLLGKIQD
                                                            YTLEDLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKP
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Pred. No. 3.9e-187;
77; Mismatches 132;
                              PAEPEVPOVETEKVEAQLKEAEVLLAKVTD
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Query Match
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Matches 519
                                                                                                                                                                                                                                                                                                                                                                                           ABQ84792 to ABQ84904 represents nucleic acids which encode the Streptococcus pneumoniae antigens given in ABP54557 to ABP54669. The S. pneumoniae antigens have antibacterial activity and can be used in vaccines. The S. pneumoniae antigens can also be used to prevent or attenuate a Streptococcal infection in an animal. The polynucleotides encoding the S. pneumoniae antigens can be used to detect Streptococcus nucleic acids. ABQ84905 to ABQ85130 represent primers used in the cloning of S. pneumoniae ORFs (open reading fra which are used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcus pneumoniae antigens, useful for Streptococcus and for preventing or attenuating di Streptococcus infection -
                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11;
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KUNSCH C A.
BARASH S C.
DILLION P J.
DOUGHERTY B.
FANNON M R.
ROSEN C A.
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                               TARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSP
                                                                           SVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSR
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RESULT 36
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                                            Claim
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UNIV MINNESOTA.
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                                                                                                                                           Finkel DJ,
: sequence is a 79 kDa protein of Streptococcus pneumoniae that is capable of degrading human complement protein C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumonia;
                                                                       human
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monia; xerotransplantation;
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(HCPC3). The sequence was deduced from the open reading frame of an isolated gene (see AAX25394). A smaller (20 kDa) HCPC3 protease is encoded by an open reading frame of S. pneumoniae serotype 3, and this open reading frame may be part of a larger open reading frame corresponding to the present sequence from the S. pneumoniae serotype 4 genome. Amino acids 1-58 and 90-132 of the 20 kDa orotein have substantial sequence identity with amino acids 170-227 and 258-300 of the 79 kDa protein. Proteins and peptides or 20 lypeptides containing these regions, and DNA sequences encoding them, are claimed. HCPC3 proteases and polypeptides can be used as immune system stimulating compositions (claimed). They can produce an immune response against infection or colonization (claimed). They can produce a B cell response, a T cell response, an epithelial cell response, or an endothelial cell response (claimed). The expression of the proteins on the surface of an organ of an animal used in xenotransplantation can be used to
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ESPEESEEPQVETEKVEEKLREAEDLLGKIQDPIIKSNAKETLTGLKNNLLFGTQDNNTI
                                           --PAEPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSI
                                                                                                                                             GWGNASEHVLGKKDHSEDPNKNFKADEE-----PVEET------
                                                                                                                                                                                                 TVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGYTLEDLLATVKYYVEHPNERPHSDN
                                                                                                                                                                                                                                        TVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSND
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e 79; Mismatches
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Best Local Similarity
Matches 419; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens at they encode a treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-452397/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pneumoniae BVH-11C protein antigen.
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YNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGK 503
                                                                                                                                                                                             ARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLK-IDSN---SSLVSQLVRKV
                                                                                                                                                                                                                                                                                                  DSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSBLEERI 327
                                                                                                                                                                                                                                                                                                                                                                                                            AEAFLSGRGNLSNSRTYRRQNSDNTSRTWWVPSVSNPGTTNTNTSNNSNTNSQASQSNDI
                                                     GDGYVFEENGVSRYIPAKNLSAETAAGIDSKLAKQESLSHKLGAKKTDLPSSDREFYNKA
                                                                                                       GEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKA 443
                                                                                                                                                                 ARII PLRYRSNHWVPDSRPEEPSPQPTPEPSPSPQPAPNPQPAPSNPI DEKLVKEAVRKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 100;
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RESULT 38
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ID AAU844029
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XX AU84
AC AAU84
XX AU84
AC AAU84
XX DH-JU
DT O8-MA
XX BY-JE
CO SYNTH
XX DPR
AC SYNTH
XX WO200
XX WO200
XX WO200
XX IS-JU
PR 20-JU
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           The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine comprising (I) is useful for therapeutic or prophylactic treatment compnising, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial
                                                                                                                                                         New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media, meningitis, and bacteraemia
                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus Synthetic.
                                                                                                                                                                                                                                                              Hamel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Truncated variant of S. pneumoniae BVH-11, BVH- version
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infection (e.g.,
                                                                                                                                Example
                                                                                                                                                                                                                                                                                                                    20-JUN-2000; 2000US-212683P
                                                                                                                                                                                                                                                                                                                                              19-JUN-2001; 2001WO-CA00908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAEKLLALLKES
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                                                                                                                             Page -; 113pp; English.
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 caused by Streptococcus
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RESULT 39
AAU84058
ID AAU8
XX
AC AAU8
XX
AC OB-N

AAU84058 standard;

Peptide; 1126 AA

AAU84058;

08-MAY-2002

(first entry)

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a truncate of a Streptococcus pneumoniae gene used to obtain antigenic peptides, described in the method of the invention.

Note: This sequence does not appear in the specification but has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus such as Streptococcus pyogenes, group B Streptococcus s
as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia
Staphylococcus aureus) in an individual susceptible to the infection.
A polynucleotide (III) encoding (I) is useful in DNA immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 AEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDI
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EAEKLLALLKES
                                EAEKLLALLKGS
                                                                   PEESEEPQVETEKVEEKLREAEDLLGKIQDPIIKSNAKETLTGLKNNLLFGTQDNNTIMA
                                                                                         PAEPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMA
                                                                                                                                       NASDHVQRNKNGQADTNQTEKPSEEKPQTEKPEEETPREEKPQSEKPESPKPTEEPEEES
                                                                                                                                                                          NASEHVLGKKDHSEDPNKNFKAD----
                                                                                                                                                                                                            VKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGYTLEDLLATVKYYVEHPNERPHSDNGFG
                                                                                                                                                                                                                                  VKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWG
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No. 8
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                                                                                                                                                                                                                                                                                            The invention describes an isolated polypeptide (I) with 70-90% CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II) CC comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection in an CC individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of sup streptococcus bacterial CC infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus pneumoniae, group A Streptococcus such as Streptococcus pneumoniae, S. uberis, S. nocardia or CC staphylococcus aureus) in an individual susceptible to the infection. CC staphylococcus aureus) in an individual susceptible to the infection. CC test for S. pneumoniae infection. (III) is useful in DNA immunisation CC test for S. pneumoniae infection. (III) is useful in a diagnostic test for S. pneumoniae infection. (III) is useful in a biological sample suspected of containing the presence of Streptococcus in a biological coused for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a chimeric consumoniae genes, described in the method of the invention but has cC been created according to information given in the invention.
                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcus pneymoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for or preventing streptococcal infections such as otitis media, meningitis, and bacteraemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hamel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pneumonia;
BVH-11-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BVH-3; BVH-11;
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 442
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                                                                                                                                                               N
                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHIRE
                                                                                                                RIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLK-IDSN---SSLVSQLVR
                                                                                                                                                                             DIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEE
                                                    KVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYD
                                                                                              RIARIIPLRYRSNHWVPDSRPEEPSPQPTPEPSPSPQPAPNPQPAPSNPIDEKLVKEAVR
 KAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERL
                                 KVGDGYVFEENGVSRYIPAKNLSAETAAGIDSKLAKQESLSHKLGAKKTDLPSSDREFYN
                                                                                                                                                              DIDSLLKQLYKLPLSQRHVESDGLIFDPAQITSRTARGVAVPHGNHYHFIPYEQMSELEK
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                                                                                                                                                                                                                                                                                            1126 AA;
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                                                                                                                                                                                                                              Conservative
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l bacterial :
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                                                                                                                                                                                                                            Score 1898; D)
Pred. No. 3.2e
63; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              otitis media; bacteraemia; infection; mutant; mutein;
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ARUSULT 40
AAU84
XX AAU84
XX AAU84
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DT O8-MA
DT O8-MA
XX BVH-1
XX BVH-1
XX STrep
OS Synth
XX W DReum
KW BVH-1
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                                                                                                                             New Streptococcus pneumoniae BVH-3 and BVH-11 veepitope-bearing polypeptides, useful as vaccine or preventing streptococcal infections such as
                                                                                                                                                                                                                                                                                                                                               Streptococcus Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                              BVH-3; BVH-11; vaccine; meningitis; pneumonia; streptococcal bacterial i
                                                                                             Example 1;
                                                                                                                                                                               WPI; 2002-122272/16.
                                                                                                                                                                                                      Hamel J,
                                                                                                                                                                                                                                                    20-JUN-2000; 2000US-212683P
                                                                                                                                                                                                                                                                                                  27-DEC-2001.
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                                                                                                                                                                                                                                                                                                                                                                                    BVH-11-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU84057 standard; Peptide; 1365
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                                                                                                                                                                                                                                                                                                                                                                                                                                pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSL 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAEAEKLLALLKGSNPSSVSKEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WGNASEHVLGKKDHSEDPNKNFKAD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAEAEKLLALLKESKGPDLTEEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESPEESEEPQVETEKVEEKLREAEDLLGKIQDPIIKSNAKETLTGLKNNLLFGTQDNNTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETPAEPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSI 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKPEEETPREEKPQSEKPESPKPTEEPEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEVKNGSLI I PHYDHYHNI KFEWFDEGLYEAPKGYTLEDLLATVKYYVEHPNERPHSDNG
                                                                                                                                                                                                     Ouellet C,
                                                                                            Page -;
                                                                                                                     and bacteraemia
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                                                                                                                                                                                                                                                                                                                                                          pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                derived chimeric peptide,
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                                                                                            English.
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                                                                                                                                                                                                       Martin
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infection; mutant; mutein;
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                                                                                                                                                       variant
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                                                                                                                                 e components for otitis media,
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The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine comprising (I) is useful for therapeutic or prophylactic treatment omeningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for

of.

therapeutic

prophylactic treatment

any

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RESULT 41
AAB12734
ID AAB12
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AC AAB12
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AC AAB12
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DI 21-NC
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DE Strep
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a chimeric gene created from fragments and variant fragments of Streptococcus pneumoniae genes, described in the method of the invention.

Note: This sequence does not appear in the specification but has been created according to information given in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection (e.g., caused by Streptococcus pneumóniae, group A Streptococcus such as Streptococcus pyogenes, group B Streptococcus such as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia or Staphylococcus aureus) in an individual susceptible to the infection. A polynuclectide (III) encoding (I) is useful in DNA immunisation
               Streptococcus
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67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEE
                                                                                                                                                                                                           MAEAEKLLALLKGS----NPSSVS
                                                                                                                                                                                                                                                           ETPAEPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSI
                                                                                                                                                                                                                                                                                                                             WGNASEHVLGKKDHSEDPNKNFKAD----
                                                                                                                                                                                                                                                                                                                                                                          VEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDG
                                                                                                                                                                                                                                                                                                                                                                                                                                     SDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEGDAYVTPHMTHSHWIKKDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAYDLLARIHODLLDNKGROVDFEALDNLLERLKDVSSDKVKLVDDILAFLAPIRHPERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAFITHPERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIARIIPLRYRSNHWVPDSRPEEPSPQPTPEPSPSPQPAPNPQPAPSNPIDEKLVKEAVR
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                                                                                                                                                                               MAEAEKLLALLKESKGPNMQPSQLS
                                                                                                                                                                                                                                     ESPEESEEPQVETEKVEEKLREAEDLLGKIQDPIIKSNAKETLTGLKNNLLFGTQDNNTI
                                                                                                                                                                                                                                                                                                                                                           VEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGYTLEDLLATVKYYVEHPNERPHSDNG
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                                                                                                                                                                                                                                                                                                  FGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKPEEETPREEKPQSEKPESPKPTEEPEE
                                           (first entry)
               pneumoniae NEW4
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                                                                                                      Protein;
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Pred. No. 1.3e-130;
               protein
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               antigen
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               SEQ
               ij
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               NO:67
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otitis media; pneumonia; immunis;
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WGNASEHVLGKKDHSEDPNKNFKAD---
                                                                                                                                                                                                        GKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSL
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                                                                                                                                                                                                                                                                                                                                                                                                                            RIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLK-IDSN---SSLVSQLVR
                                                         VEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDG
                                                                                                        SEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYT
                                                                                                                                                                                 GKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEGDAYVTPHMTHSHWIKKDSL
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                                                                                                                                                                                                                                                                        infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus syogenes, group B Streptococcus such as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia or Staphylococcus aureus) in an individual susceptible to the infection. A polynucleotide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a truncate
                                                                                                Sequence
                                                                                                                                                                                                                    of a Streptococcus pneumoniae gene used to obtain antigenic peptides, described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page -; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             meningitis, and bacteraemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-122272/16
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                                                                                                                                                                                              Note: This sequence does
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention describes an isolated polypeptide (I) with 70-90% atity to Streptococcus pneumonia protein BVH-3, BVH-11, vari
                                                                                                                                                          This sequence does not appear in the specification but has created according to information given in the invention.
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            WPI; 2002-122272/16
                                    Hamel J,
                                                                                                                                          27-DEC-2001
                                                                                                                                                                                                       Streptococcus pneumoniae
                                                                                                                                                                                                                                 pneumonia;
                                                                                                                                                                                                                                              BVH-3; BVH-11; vaccine;
                                                                                                                                                                                                                                                                      Truncated variant of S. pneumoniae BVH-11, NEW24.
                                                                                                                                                                                                                                                                                                 08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                 AAU84031 standard; Peptide; 612
                                                                                      20-JUN-2000; 2000US-212683P
                                                                                                               19-JUN-2001; 2001WO-CA00908
                                                                                                                                                                  WO200198334-A2
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                                                             SHIRE BIOCHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIARIIPLRYRSNHWVPDSRPEEPSPQPTPEPSPSPQPAPNPQPAPSNPIDEKLVKEAVR
                                                                                                                                                                                                                                                                                                                                                                                                                   MAEAEKLLALLKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDG 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEGDAYVTPHMTHSHWIKKDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAYDLLARIHQDLLDNKGRQVDFEALDNLLERLKDVSSDKVKLVDDILAFLAPIRHPERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVGDGYVFEENGVSRYIPAKNISAETAAGIDSKLAKQESISHKIGAKKTDIPSSDREFYN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYD 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLK-IDSN---SSLVSQLVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIDSLLKQLYKLPLSQRHVESDGLIFDPAQITSRTARGVAVPHGNHYHFIPYEQMSELEK
                                                                                                                                                                                                                                                                                                                                                                                                                              MAEAEKLLALLKGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESPEESEEPQVETEKVEEKLREAEDLLGKIQDPIIKSNAKETLTGLKNNLLFGTQDNNTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETPAEPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKPEEETPREEKPQSEKPESPKPTEEPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEVKNGSLI I PHYDHYHNI KFEWFDEGLYEAPKGYTLEDLLATVKYYVEHPNERPHSDNG
                                    Ouellet C,
                                                                                                                                                                                                                               -11; vaccine; meningitis; otitis media; bacteraemia; streptococcal bacterial infection; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                 (first entry)
                                     Charland N,
                                                                                                                                                                                                                                                                                                                                                                                                                  554
                                                                                                                                                                                                                                                                                                                                                                                                                                          785
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                                       Martin
                                     'n
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                                       Brodeur
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a truncate of a Streptococcus pneumoniae gene used to obtain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of a Streptococcus pneumoniae gene used to obtain antigenic described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: This sequence does not appear in the specification but has been created according to information given in the invention.
                                                                                              692
                                                                                                                                           416
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                                                                                                                                                                                                                                  YAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLII
                                                                                                                                                                                                                                                                                                                                                          EDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQA
                                                                                                                                                                                                                                                                                                                                                                                                                             PLSERHVESDGLIFDPAQITSRTARGVAVPHGNHYHFIPYEQMSELEKRIARIIPLRYRS
                                            NKADQDSKPDEDKEHDEVSEPTHPESDEKENHAGLNPSADNLYKPSTDTEETEEEAEDTT
                                                                                                                                                                                                                                                                                 YTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAFITHPERLGKPNSQIEYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGVSRYIPAKDLSAETAAGIDSKLAKQESLSHKLGAKKTDLPSSDREFYNKAYDLLARIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NHWVPDSRPEQPSPQSTPEPSPSLQPAPNPQPAPSNPID--EKLVKEAVRKVGDGYVFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NHWVPDSRPEQPSPQPTPEPS-----PGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGKQGSRPSSSSYNANFVQPRLSENHNLTVTPTYHQ-----NQGENISSLLRELYAK
AEPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAE
                                                                                                                                        PHYDHYHNIKFEWFDEGLYEAPKGYSLEDLLATVKYYVEHPNERPHSDNGFGNASDHVRK
                                                                                                                                                                                                                                                                                                                                 DDEIQVAKLAGKYTTEDGYIFDPRDITSDEGDAYVTPHMTHSHWIKKDSLSEAERAAAQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and bacteraemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1808; DB 23;
Pred. No. 5.7e-125;
8; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                            -DPNKNFKADEEPVEETP
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Best Local S
Matches 345
                                                                                                                                                                                                                                                                 antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the protein they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcal otitis media,
                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                        S. pneumoniae NEW10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        otitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB12741 standard;
                                                                                                                                                                                                                                                                                                                                                      The present invention describes nucleic acids
                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Fig 39; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hamel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-DEC-1999;
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               440
                                                             380
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                                                                                                                                                       266 DIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      media;
                                                                                                                                   2 NISSLLRELYAKPLSERHVESDGLIFDPAQITSRTARGVAVPHGNHYHFIPYEQMSELEK
                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOCHEM PHARMA
RIARIIPLRYRSNHWVPDSRPEQPSPQSTPEPSPSLQPAPNPQPAPSNPID--EKLVKEA
                                                                                                           RIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPS----PGPQPAPNLKIDSNSSLVSQL
                                     VRKVGDGYVFEENGVSRYIPAKDLSAETAAGIDSKLAKQESLSHKLGAKKTDLPSSDREF
                                                       VRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEF
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                                                                                                                                                                                                                                 568
                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      antigens useful for bacteremia and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumonia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0113800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-CA01218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                         protein antigen
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                                                                                                                                                                                           43.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pineau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              568
                                                                                                                                                                                Score 1795.5; DB 2
Pred. No. 4.3e-124;
1; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                 for
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antigens
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RESULT 45
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                                                                                            The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BWH-11, variants of BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial
            Streptococcus such as Streptococcus as Streptococcus agalactiae, S. dysc
                                                                                                                                                                                                                                                                                                                                                      Example 1; Page -; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for or preventing streptococcal infections such as otitis media, meningitis, and bacteraemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-122272/16.
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                                                                      infection (e.g.,
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caused by Streptococcus pneumoniae, group A ich as Streptococcus pyogenes, group B Streptococcus such agalactiae, S. uberis, S. nocardia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of S. pneumoniae
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RESULT 46
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AC AAU84
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XX 08-MA
XX DF S. pn
XX BVH-3
KW Dreum
KW BVH-1

08-MAY-2002

entry)

AAU84055

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Peptide;

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S. pneumoniae

derived (first

chimeric

peptide,

NEW28

otitis media; bacteraemia;

mutant;

pneumonia; BVH-11-2.

BVH-3; BVH-11; vaccine; meningitis; pneumonia; streptococcal bacterial i

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Best Local S
Matches 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a truncate of a Streptococcus pneumoniae gene used to obtain antigenic peptides, described in the method of the invention.

Note: This sequence does not appear in the specification but has been created according to information given in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus) in an individual susceptible to the infection. A polymucleotide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPS-----PGPQPAPNLKIDSNSSLVSQL 379
LGTKDNNTISAEVDSLLALLKESQPAPI
                   LQIMDNNSIMAEAEKLLALLKGSNPSSV
                                                           TEETEEEAEDTTDEAEIPQVENSVINAKIADAEALLEKVTDPSIRQNAMETLTGLKSSLL
                                                                                                                                                            DGWGNASEHVLGK---
                                                                                                                                                                                          YTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGYSLEDLLATVKYYVEHPNERPHSD
                                                                                                                                                                                                                                                                         SLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVE
                                                                                                                                                                                                                                                                                                                                     RLGKPNSQIBYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRKVGDGYVFEENGVSRYIPAKDLSAETAAGIDSKLAKQESLSHKLGAKKTDLPSSDREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIARIIPLRYRSNHWVPDSRPEQPSPQSTPEPSPSLQPAPNPQPAPSNPID--EKLVKEA 119
                                                                                           FKADEEPVEETPAEPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLT 762
                                                                                                                          NGFGNASDHVRKNKADQDSKPDEDKEHDEVSEPTHPESDEKENHAGLNPSADNLYKPSTD
                                                                                                                                                                                                                                                       SLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQ
                                                                                                                                                                                                                                                                                                                      RLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEGDAYVTPHMTHSHWIKKD
                                                                                                                                                                                                                                                                                                                                                                                     YNKAYDLLARIHQDLLDNKGRQVDFEVLDNLLERLKDVSSDKVKLVDDILAFLAPIRHPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1795.5; DB 2:
Pred. No. 4.3e-124;
1; Mismatches 107;
                                                                                                                                                            KDHSE---
                               790
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a chimeric gene created from fragments and variant fragments of Streptococcus pneumoniae genes, described in the method of the invention.

Note: This sequence does not appear in the specification but has been created according to information given in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BVH-3 of BVH-11, or chimeric sequences derived from them. A vaccine (II) comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus aureus) in an individual susceptible to the infection. A polymaclectide (III) encoding (I) is useful in DNA immunisation techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hamel J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-2001; 2001WO-CA00908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page -; 113pp; English
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241
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                         RLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKD
                                                                     YNKAYDLLARIHQDLLDNKGRQVDFEVLDNLLERLKDVSSDKVKLVDDILAFLAFIRHPE
                                                                                                                                               VRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEF
                                                                                                                                                                                                                             RIARIIPLRYRSNHWVPDSRPEQPSPQSTPEPSPSLQPAPNPQPAPSNPID--EKLVKEA
                                                                                                                                                                                                                                                     RIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPS-----PGPQPAPNLKIDSNSSLVSQL
                                                                                                                                                                                                                                                                                                       NISSLLRELYAKPLSERHVESDGLIFDPAQITSRTARGVAVPHGNHYHFIPYEQMSELEK
RLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEGDAYVTPHMTHSHWIKKD
                                                                                                           YDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1139 AA;
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     43.1%; Score 1795.5; DB 2 60.7%; Pred. No. 1.3e-123;
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RESULT. 47
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Infection (e.g., caused by Streptococcus preumoniae, group A Streptococcus such as Streptococcus progenes, group B Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia Staphylococcus aureus) in an individual susceptible to the infection. A polynucleotide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus nolymentiae.
                                                                                       The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (I but is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial
                                                                                                                                                                                                                                                              New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components or preventing streptococcal infections such as otitis medi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
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    pneumoniae

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                                                                                                                                                                                                                    Example 1;
                                                                                                                                                                                                                                                  meningitis, and bacteraemia
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                                                                                                                                                                                                                                                                                                                                                        Hamel J,
                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-2000; 2000US-212683P
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                                        Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal.
                                                                                                                                                                                           AAB12728
            Streptococcus
                                                                                                    Streptococcus
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                                                                                                                                                                                           standard;
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            pneumoniae
                                                                                                 pneumoniae BVH-11A protein antigen
                                                                                                                                                                                           Protein;
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Pred. No. 1.7e.
71; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, ortis media, bacteraemia and/or pneumonia. The present sequence represents the S. pneumoniae BVH-11A protein antigen.
                        BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia; pneumonia; streptococcal bacterial infection; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hamel J,
                                                                                                          Truncated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYELGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSNPGTTNTNTSNISNTNISQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ARGVAVPHGDHYHFIPYSQMSELEERIARIIPL 333
                                                                                                                                                                                                                                                                                                                                                                                                       ARGVAVPHGNHYHFI PYEQMSELEKRIARI I PL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLIFDPAQITSRT
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                                                                                                        variant of S.
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                                                                                                                                                                                                                                                                 Peptide;
                                                                                                                                                            entry)
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                                                                                                     pneumoniae BVH-11, BVH-11A.
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Pred. No. 7.2e-115;
9; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     meningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus progenes, group B Streptococcus such as Streptococcus pyogenes, group B Streptococcus such as Streptococcus autreus) in an individual susceptible to the infection.

C Staphylococcus autreus) in an individual susceptible to the infection.

C A polynucleotide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcus pneumoniae gene used to obtain antigenic peptides, described in the method of the invention.

C Note: This sequence does not a pnear in the specification but has
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Sim
Matches 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epitope-bearing polypeptides, or preventing streptococcal in meningitis, and bacteraemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hamel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page -; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Streptococcus pneumoniae BVH-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200198334-A2
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                                                                                GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
                                                                                                                                               AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT
                                                                                                                                                                                                                              SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA
    VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
                                                                                                                                                                                                SHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVNGKYYVYLKDA
                                                                                                                                                                                                                                                                             AYELGLHQAQTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVT
                                                                                                                       AHADNVRTKEEINRQKQEHSQHREGGTSANDGAVAFARSQGRYTTDDGYIFNASDIIEDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide (I) with 70-90% protein BVH-3, BVH-11, variants of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as vaccine
                                                                                                                                                                                                                                                                                                                                                        .2e-115;
les 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e components for treating otitis media,
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                                                                                                                                                                                                                                                                                                                                                                                            Length
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RESULT 50
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밁
                           techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the process of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a chimeric gene created from fragments and variant fragments of Streptococcus pneumoniae genes, described in the method of the invention.

Note: This sequence does not appear in the specification but has been created according to information given in the invention.
                                                                                                                                                                                                                 BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II) comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus group B Streptococcus such as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia or Staphylococcus aureus) in an individual susceptible to the infection. A polynucleotide (III) encoding (I) is useful in DNA immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media, meningitis, and bacteraemia -
Sequence
                                                                                                                                                                                                                                                                                                                                                                                         identity to Streptococcus pneumonia protein BVH-3, BVH-11, BVH-3 or BVH-11, or chimeric sequences derived from them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page -; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-122272/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-2001; 2001WO-CA00908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BVH-3; BVH-11; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S. pneumoniae derived chimeric peptide, NEW29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUN-2000; 2000US-212683P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pneumonia;
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                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes an isolated polypeptide (I) with 70-90%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SHIR-) SHIRE BIOCHEM INC.
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Query Match Best Local Matches 314;

Local Similarity

39.9%;

Score 1661; DB 23, Pred. No. 1.3e-113;

Indels

4;

Gaps

Conservative

57;

Ü	2 DIDSLLKQLYKLPLSQRHVESDGLIFDPAQITSRTARGVAVPHGNHYHFIPYEQMSELEK 61
•	326 RIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLK-IDSNSSLVSQLVR 381
Ū	62 RIARIIPLRYKSNHWVPDSRPEEPSPQPTPEPSPSPQPAPNPQPAPSNPIDEKLVKEAVR 121
	382 KVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYD 441
Ū	122 KVGDGYVFEENGVSRYIPAKNLSAETAAGIDSKLAKQESLSHKLGAKKTDLPSSDREFYN 181
	442 KAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERL 501
Ū	182 KAYDLLARIHQDLLDNKGRQVDFEALDNLLERLKDVSSDKVKLVDDILAFLAPIRHPERL 241
`	502 GKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSL 561
Ū	242 GKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEGDAYVTPHMTHSHWIKKDSL 301
	562 SDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHT 621
Ü	302 SEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYT 361
`	622 VEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDG 681
Ü	362 VEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGYTLEDLLATVKYYVEHPNERPHSDNG 421
	682 WGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKE 733
Ū	422 FGNASDHVGPNMQPSQLSYSSTASDNNTQSVAKGSTSKPANKSENLQSLLKE 473
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1 SYELGLYQARTVKENNRVSY.....KLLALLKGSNPSSVSKEKIN
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A; Lettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heion, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001

A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A; Reference number: A95000; MUID:21357209; PMID:11463916

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C;Superfamily:
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A;Molecule type: DNA
A;Residues: 1-802 <KUR>
A;Cross-references: GB:AE005672; PI
A;Experimental source: strain TIGR4
C;Genetics:
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             NRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLED
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                                                   EGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIY
                                                                 EGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIY
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hypothetical protein phtA [imported] - Streptococcus pneumoni C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_chan C;Accession: E98004
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; B. e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Mat y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; B. A;Title: Genome of the Bacterium Streptococcus pneumoniae Str. A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: E98004
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A;Cross-references: GB:AE007317; PIDN:AAK99865.1; PID:g15458683; GSPDB:GN00174
C;Genetics:
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C;Superfamily: Streptococcus agalactiae hypothetical 92.4K protein
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Pred. No. 3e-219;
0; Mismatches
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Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren,
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RESULT 3
D98004
histidine Motif-Containing protein [imported] - Streptococcus pneumoniae (strain C;pecies: Streptococcus pneumoniae
C;pecies: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C;Accession: D98004
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren Y, P.; Sun, P.M.; Winkler, M.E.
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; pMID:11544234
A;Accession: D98004
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A;Molecule type: DNA
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C; Superfamily:
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                                                                                                                                GDAYIVPHGDHYHYIPKNELSASELAAAKAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
                                                                                                                                                  GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
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                                                              VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLIFDPAQITSRT
                                                                                       VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
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75.0%;
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Pred. No. 3.2e-
69; Mismatches
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8.2e-168;
les 99;
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train R6.
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A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus, A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: B95136
A;Accession: B95136
                                                                                                                                                                                                                                                                        A;Status: preliminary
A,Molecule type: DNA
A,Residues: 1-819 < KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75283.1;
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1174
C;Superfamily: Streptococcus agalactiae hypothetic
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B95136
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001
C;Accession: B95136
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen,
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               AAHADNIRTKEEIKRQKQERSHNHNS---
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                                                                                TSHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVNGKYYVYLKD
                                                                                                                                                                                                                                                                                 Streptococcus agalactiae hypothetical 92.4K
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               RADNAVAAARAQGRYTTDDGYIFNASDIIED
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A; Accession.
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-839 < KUR>
A; Cross-references: GB: AE005672; PII
A; Cross-references: GB: AE005672; PII
                                                                                                                                                                                                                           nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95115
                                                                                                                                                                                                                                                                                                                                                     RESULT 5
G95115
G95116
Conserved hypothetical protein SP1003 [imported] -
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001
C;Accession: G95115
C;Accession: G95115
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen,
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                                                                                                   Streptococcus agalactiae hypothetical
                                    Conservative
                                                    66.6%;
                                    91; Mismatches 144;
                                                                                                                                                                   PIDN: AAK75120.1;
                                                    Score 2772;
Pred. No. 1.
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hypothetical protein phtD [imported] - Streptococcus pneumoniae (strain R C.)Species: Streptococcus pneumoniae
C.)Species: Streptococcus pneumoniae
C.)Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-20
C.)Accession: C97985
R.;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.;
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.;
y, P.; Sun, P.M.; Winkler, M.E.
y, P.; Sun, P.M.; Winkler, M.E.
y, P.; Sun, P.M.; Winkler, M.E.
A; Hitle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Recession: C97985
A;Accession: C97985
A;Residues: 1-853 <KUR> RESULT C97985

02-Nov-2001 (strain

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A;Cross-references: (C;Genetics: C;Genetics: A;Gene: phtD C;Superfamily: Strep
RESULT 7
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conserved hypothetical protein SP1004 [imported] - Streptococcus pneumoniae (strain
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                                                                                                                                                       EEDKEHDEVSEPTHPESDEKENHVGLNPSADNLYKPSTDTEETEEEAEDTTDEAEIPQVE
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Pred. No. 2e-141;
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on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, I nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001

A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus, A; Reference number: A95000; MUID:21357209; PMID:11463916

A; Scatus: preliminary
A; Molecule type. Two
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A;Residues: 1-1039 <KUR>
A;Cross-references: GB.AE005672; PIDN:AAK75121.1; PID:gl4972477; GSPDB:GN00164;
A;Experimental source: strain TIGR4
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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  IDEH - - - KPVGIG - - -
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                                           FDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDG----WGNASEHVLGKKDHSEDPN
                                                                                          EQDYPSNAKEMKDLDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIIYPHGDHHHADP---
                                                                                                                                                                                                                                                                                  QPTLPNNSLATPSP-SLPINPGTSHEKHE-----
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  HSHSNYELFKPEEGVAKKEGNKVYTGEELTNVVNLLKNSTFNN
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Pred. No. 3.6e-60;
7; Mismatches 180
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RESULT 8
D97985
hypothetical protein phtE [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C;Accession: D97985
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.?
R;Hoskins, J.A.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, P.; P.; Sun, P.M.; Winkler, M.E.
Y, P.; Sun, P.M.; Winkler, M.E.
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A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas,
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: D97985
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A;Molecule type: DNA
A;Residues: 1-1039 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYELGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVT
WFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDG----WGNASEHVLGKKDHSEDP
                                   HEQDYPGNAKEMKDLDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIIYPHGDHHHADP--
                                                                                                                                                 DEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTG-DSAAA
                                                                                                                                                                                           QPTLPNNSLATPSP.
                                                                                                                                                                                                                                                                    ----LTTSKELSSASDGYIFNPK-DIVEETATAYIVRHG--DHFHYIPK-----SNQIG
                                                                                                                                                                                                                                                                                                        VSHTLTAKKENVAPROQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTN
                                                                                                                                                                                                                                                                                                                                                                                  PQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQES
                                                                                                                                                                                                                                                                                                                                                                                                                            PNGVAIPHGDHYHFIPYSKLSALEEKIARRVP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNAYIVPHGGHYHYIPKSDLSASELAAAKAHLAGKNMQPSQLSYSSTASDN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHADNVRTKDEINROKOEHVKDNE----KVNSNVAVARSOGRYTTNDGYVFNPADIIEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHGDHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTPDQVSQKEGIQAEQIVIKITDQGYVT
                                                                                                                 EDESGFIMSHGNHNHYFFKKDLTEEQIKAAQKHLEE---
                                                                                                                                                                                                                           KEKLVDDLLAFLAPITHPERLGKP-NSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIIS
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                                                                                                                                                                                                                                                                                                                                                ISGTGSTVSTNAK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.8%; Score 1243; DB 2;
41.2%; Pred. No. 5.2e-60;
tive 94; Mismatches 180;
                                                                                                                                                                                           ----SLPINPGISHEKHE
                                                                         EKRIPLVRLPYMV--EHTVEVKNGNLII-PHKDHYHNIKFA
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                                                                                                                 ----VKTSHNGLDSLSS
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                                                                                                                                                                                         -EDGYGFDANRIIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical 92.4K protein - Streptococcus agalactiae C;Species: Streptococcus agalactiae C;Species: Streptococcus agalactiae C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000 C;Accession: T46758
R;Spellerberg, B.; Rozdzinski, E.; Martin, S.; Weber-Heynemann, J.; Schnitzl Infect. Immun. 67, 871-878, 1999
A;Title: Lmb, a protein with similarities to the LraI adhesin family, mediat A;Reference number: Z24091; MUID:99115568; PMID:9916102
A;Accession: T46758
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A;Cross-references: EMBL:AF062533; NID:g4249622; PIDN:AAD13797.1;
A;Experimental source: strain R268
C;Superfamily: Streptococcus agalactiae hypothetical 92.4K protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYQLGKHHMGLATKDNQIAYIDDSKGKVKAPKT-NKTMDQISABEGISAEQIVVKITDQG
VKAKGQADELVAALDQEQGKEKPLFDTKKVSRKVTKDGKVGYIMPKDGKDYFYARYQLDL 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPAPGRRKAP-IPDVTPNPGQGHQPDNGGYHPAPPRPNDASQNKHQRDEFKGKTFKELLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPGSKRKNIRTKQQIAEQVAKGTKEAKEKGLAQVAHLSKEEVAAVNEAKRQGRYTTDDGY
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                                                                                                                                                                                                                                                    GISRYVFAKDLÞSETVKNLESKLSKQESVSHTLTAKKENVAÞRDQEFYDKAYNLLTEAHK 452
                                                                                                                                                                                                                                                                                                                                                                                    QLHRLDLKYRHVEEDGLIFEPTQVIKSNAFGYVVPHGDHYHIIPRSQLSPLEMELAD---
                                                                                                                                                                                                                                                                                                                                                                                                            QLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QNSDNTSRTNWVPSVS-NPGTTNTNTSN-----NSNTNSQASQSND-----IDSLLK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDAAHADNVRTKEEINRQKQEHSQH-REGG------TPRNDGAVALARSQGRYTTDDGY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YVTSHGDHYHFYNGKVPYDAIISEELLMTDPNYHFKQSDVINEILDGYVIKVNGNYYVYL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYL 117
                                 TKEKG----ILPPSPDADVKANPTGDSAAA--
                                                                                                                                                                                         ALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTE 512
                                                                                                                                                                                                                                                                                                                                                LRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEK 392
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                                                                                                               DEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFSPTDIIDDLGDAYLVPHGNHYHYIPKKDLSPSELAAAQAYWSQKQGRG--ARPSDYRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLS---GRGNLSNSRTYRR 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.4%; Score 934; DB 2; 29.4%; Pred. No. 2.7e-43;
                                                                           YDTSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANW
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                                                                                                                                                       -----GKP-----
                                       --IYNR----
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Indels Length

245;

736 74 35;

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168 775 128

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-NNNINYNNIGOR

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332 941

-LSEPTTTTKKD

1123

SRDETKELE

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1198 624 1156

673

b 722

1242

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1078

505

1027

391 988

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R;HOSKINS, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, Be, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: F97985
trfA protein - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t
C;Accession: T14004
R;Saito, J; Adachi, H.; Sutch, K.
J. Biol. Chem. 273, 24654-24659, 1998
A;Title: Dictyostelium TRFA homologous to yeast Ssn6
                                                                                                                                  RESULT
T14004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-182 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein phtE-truncation [imported] - Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001 C;Accession: F97985
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Matches 61
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                                                                                                                                                                                                                                            IARIIPLRYRSNH
                                                                                                                                                                                                                                                                                 V-----LSNPSLHVHHEEEDGHGFDANRIISEDSEGFVIPHGDHNHYIKV-QTKGYEAA
                                                                                                                                                                                                                                                                                                                     IDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEER
                                                                                                                                                                                                                                                                                                                                                                                            AAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSND
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Pred. No. 1.5e-06;
6; Mismatches 50;
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A;Accession: T14004
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1390 <SAI>
A;Cross-references: EMBL:AB009080; NID:d1228566; PID:d1(C;Genetics:
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A;Residues: 1-1271 <BOR>
A;Cross-references: EMBL.M59706; NID:g160311; PID:g160312
A;Note: sequence extracted from NCBI backbone (NCBIN:77801,
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                                                                                                                                          VKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEH-TVEVKNGNLIIPHKDHYHNIKFAWF
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                   -QHEIVEVEEILPEDKNEKVQHEIVEVEEILPEDKNEKGQHEIVEVEEILPEEDKNEKGQ
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A;Residues: 1-2481 «KUD»
A;Cross-references: GB:BA000018; PID:g13701961;
A;Experimental source: strain N315
C;Genetics:
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C;Accession: D90011
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C;Species: Staphylococcus aureus
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                                                                                 DNTTGATTEE-----KNAAKDLVLKAKEKAYQDILNAQTTNDVTQIKDQAVADIQGITAD 1433
                                                                                                                                                                                                                                                                                                                                       QEIQATPDATDEEKQAADAEANTENGKA---
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                                     ITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSH 554
                                                                                                                        DKAYNLLTEAHKALFXNKGRNSDFQALDKLLER-LNDESTN-----KEKLVDDLLAFLAP
                                                                                                                                                                  ITAATDDNGVDT----AKDAGKNSIQSTQPATAVKSNAKNEVDQAVTTQNQAI------
                                                                                                                                                                                                        --YVFEEKGISRYVFAKDLPSETVKNLES----KLSKQESVSHTLTAKKENVAPRDQEFY 440
                                                                                                                                                                                                                                                    EAAINAVTPKVVKKQAAKDEIDQLQATQTNVINNDQNATNEEKEAAIQQLATAVTDAKNN 1329
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19.4%; Pred. No. 0.5;
htive 140; Mismatches
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A; Residues: 1-1233 < MUR>
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A; Accession: S56271
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C;Bpecies: Saccharomyces cerevisiae
C;Bate: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 19-Apr-2002
C;Accession: S56271
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                                                                                                          PSVLAKNQKETEIGKEDHVFEQKDKEDEKCRKELSVNHENNMSHNFNAAGSDSIIPPETE
                                                                                                                                                              HGLEAGDE----NGQASTKDVESESLTKNGFNFKENESKHLKAGEKQQTE---SDRDGIS
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 QEAVRNNEVSGTEEESTSKGEEIMGGD
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                                                     DDETMGPTKRISDNEKNLQHGTNDISVEVEKEEEEEEEEEENSTFSKVKKENVTGE
                                                                               -DSLLKQLYKLPLSQRHV---------ESDGLVFDPAQ---ITSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.; Hagiwara, H.;
Data Library, May 19
of the nucleotide
                                                                                                                                                                                                                                                                                                                                                                                               4.1%; Score 171; DB 2; 19.8%; Pred. No. 0.21;
                         -TARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSN-----
                                                                                                                                                                                                                                                                                                                                                                                    142;
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                                                                                                          AVTKEDENMENSKIAEALKDVTGDQEIDDINISDEFQRTVELPELEKQDIKDNKGEDKEL
                                                                                                                                                                  --HSEDPNKNFKADEEPVEETPAEPEVPQVE----TEKVE-AQLKEAEVLLAKVTDSSL
                                                                                                                                                                                                                             DAPKEAEVTAELNKENEDVEVAATSKEDIETKCSEPAETPIED----GTCTEAEVSKKDAE
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                                                  KANATETLAGI -----RNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSVSKEKIN 796
                                                                                                                                                                                                                                                                                  KAPN--GYTLE------DLFATIKYYVE----HPDERPHSNDGWGNASEHVLGKKD--
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C;Accession: D84900
C;Accession: D84900
C;Accession: D84900
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. R;Lin, X.; Kaul, S.; Cronin, L.A.; Shea, M.; VanAken, S.E.; Umayam, L.; Tallon, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-766, 1999 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1043 <STO> A;Title: Sequence and analysis of chromosome A;Reference number: A84420; MUID:20083487; Ph. A;Accession: D84900 hypothetical protein At2g46240 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 A;Gene: At2g46240 A;Map position: 2 A; Cross-references: Query Match Best Local Sim Matches 169; ;Genetics: 349 143 271 40 Similarity REGGTP---IVNEVKGGYVIKVDGKYYVYLKDAAHADNVRTKEEI----KESSNEGRNLESCPSDLHRNEGQITQAKGK-----EGNFECNVLSDAEEKSSVINIPVAN KREGINAEQIVIKITDQGYVTSHGDHYHYYNGKV---PYDAIISEELLMKDPNYKLKDED KRDDVEASE Conservative GB:AE002093; 4.0%; 18.5%; 108; -RNDGAVALARSOGRYTTDDGYIFNASDIIEDTGDAYIVPHGD 190 NID:g3702325; PIDN:AAC62882.1; Score 168.5; D Pred. No. 0.22; 8; Mismatches -SSNEDRKKMQNGKTVEYPFDISMIKSL--------QDVKEAQNQKNKEEPGQVPYPIFWIPSYGKRKDVEASES ne 2 of the plant Arabidopsis thaliana PMID:10617197 BB 327; 2 Indels Length -----NRQKQEHSQH 142 1043; GSPDB:GN00139 Gaps 96 403 348 306 η, _L

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RESULT 16
G89957
C;Species: Staphylococcus aureus
C;Apecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Apecies: 10-May-2001 #sequence, revision 10-May-2001 #text_change 22-Oct-2001
C;Apccession: Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Tnoue, R.; Kaito, C.; Sekimizu,
R., A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: G89957
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-891 <KUR>
A;Cross references: GB.BA000018; PID:gl3701526; PIDN:BAB42820.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
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                                                                                  HIADKUNHTGKAAKLDVVKQNYNNTDKVTDKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYD-KAYN---LLTEAH 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STVEPATVIFTKTGPVIELGLKTASTWKKFEVYEGDKKLPVELVSYDSDKDYAYIRFPVS
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                                                                                                                     QIMDNNSIMAEAEKLLALLKG-SNPSSVSKEK
                                                                                                                                                                                         VPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNL------
                                                                                                                                                                                                                                             ADVIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KALFXNKGRNSDFQALDKLLERLNDE-STNKEKLVDDLLAFLA-----PITHPERLGKPN 505
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                                                                                                                                                                                                                                                                                  FATIKYYVEHPDERPHSN----DGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPE
                                                                                                                                                                                                                                                                                                                       EGQYHVRIINQDINTKDDDTSQNNTSEPLNVQTGQEGKVADTDVAENSSTATNPKDASDK
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                                                                                                                                                            -KYDLKEMDTQIAKDTDRNV-----DNSVGMSSNVDTDKDSNKNKDKVIQLA 787
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                                                                                                                                                                                                                                             - PESDVVKDADNNIDKDVQHDVDHLSDMSDNNHFD
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A;Molecule type: mRNA
A;Residues: 1-1420 <STA>
A;Residues: 1-1420 <STA>
A;Cross-references: EMBL:Z14997; NID:g64551; PIDN:CAA78718.1; P
A;Experimental source: A6 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:121141)
C;Complex: This.protein is part of a large molecular complex.
C;Function:
A;Description: may be the amiloride-sensitive component of the
C;Superfamily: amiloride-sensitive sodium channel Apx protein
C;Keywords: glycoprotein; membrane-associated protein; sodium t;Keywords: glycoprotein; membrane-associated protein; sodium t;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amiloride-sensitive sodium channel Apx protein - African clawed frog N;Alternate names: apical plasma membrane protein C;Species: Xenopus laevis (African clawed frog) C;Date: 30-Apr-1993 #sequence_revision 19-Oct-1995 #text_change 22-Jun-1999 C;Accession: A44361; S25517 R;Staub, O.; Verrey, F.; Kleyman, T.R.; Benos, D.J.; Rossier, B.C.; Kraehenl J. Cell Biol. 119, 1497-1506, 1992 A;Title: Primary structure of an apical protein from Xenopus laevis that par A;Reference number: A44361; MUID:93107151; PMID:1334959 A;Accession: A44361
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Matches 180
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Keywords: glycoprotein; membrane-associated protein; sodium transport; 
119,462,481,503,660,664,988,1038,1211,1273/Binding site: carbohydrate
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                                                                                                                                                                                                                                                                              NLLTEAHKALF-----XNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPE
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  SAYLQTKNSADSSYKKDDTEKVAVTRIGGRKRI--
                                                                            SLMNDYIEKLKVAQKKVLRETSFKRKDLQMSLPCRFKLNPPKRPTIDHFRSYSSSSANEE
                                                                                                                      SLS----DKEKVAAQAYTKEKGI----LPPSPDADVKANP---
                                                                                                                                                            KLPKNKS.
                                                                                                                                                                                                                                          HLAGGRHSAFIAPVHNTNPAQQEKLKLESKTLERMNNIS
                                                                                                                                                                                                                                                                                                                        -----FQKDATVKSIPLLSQQLQQEKCKSHPL-----SDLNCEKITKASTPMLY
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                                      TGDSAAAIY----
                                                                                                                                                          3.9%; Score 161; DB 1; 19.8%; Pred. No. 0.89;
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                                      NRVKGEKRI PLVRL PYMVEHTVEVKNGNL I I PHK-D
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A;Molecule type: DNA
A;Residues: 1-2810 <WIL>
A;Residues: 1-2810 <WIL>
A;Cross-references: EMBL:Z66563; PIDN:CAA91469.1; GSPDB:GN00028; CESP:F46C3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Cottage, A.
submitted to the EMBL Data Library,
a.Reference number: Z19543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F46C3.3 - Cae
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_rev
C;Accession: T22298
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A;Map position: X
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A;Accession: T22298
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A; Introns: 67/2
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1958/3; 1999/1; 2078/1;
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                                                                                                                                                                             ASQSNDI-----DSLLKQLYKLP-LSQRHVESDGLVFDPAQITSRTARGVAVPHG
                                                                                                                                                                                                                 VASEHKAQ-
                                                                                                                                                                                                                                                         SASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQ
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                                                           P
                                                                                             DHYHFIPYSQMSELEER-----IARIIP--LRYRSNHWV--PDSRPEQPSPQPT-----
                                                                                                                                       RSPSVDILKPPMSRRTPDAMVEQTYVRPHLAQSPV-
                                                                                                                                                                                                                                                                                                   DDQMNYRTRSRERSLPRFHSNNGYNYDPSQPV----YMMPVQMNGHGEMILLSP----
                                                                                                                                                                                                                                                                                                                                         GTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVP-----HGDHYHYIPKNEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.8%; Score 159; DB
18.5%; Pred. No. 3.1;
ative 137; Mismatches
                                                         SRARERMENPLLARQIPRAYPYQNGNVVPPPPSSYRAPSPAPTSGDRRG 1901
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                                                                                                                                       --GRQTSRFEEFSALPRG
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3.8%; Score 158; DB 2; Length 1 17.7%; Pred. No. 1.6; tive 127; Mismatches 311; Indels YDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVD ::	RESULT 19 T1844 Appothetical protein C0385c - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000 C;Accession: T18444 R;Lawson, D.; Bowman, S.; Barrell, B. submitted to the EMBL Data Library, August 1997 A;Reference number: Z18935 A;Reference number: Z18935 A;Accession: T18444 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Rotous: 1-1650 <law> A;Cross-references: EMBL:Z98547; NID:e1325376; PID:e1427940; PIDN:CAB11112.2</law>	
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996 A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae A;Reference number: \$73327; MUID:97105885; PMID:8948633 A;Accession: \$73361 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-910 <him> A;Cross-references: EMBL:AE000004; GB:U00089; NID:g1673671; PIDN:AAB95683.1; PID:g167368 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996 C;Genetics: A;Genetic code: SGC3 C;Superfamily: Mycoplasma heat shock protein dnaJ homolog C09_orf910; dnaJ amino-termina F;7-71/Domain: dnaJ amino-terminal homology <dnj> Query Match Best Local Similarity 19.0%; Pred. No. 0.77; Matches 161; Conservative 127; Mismatches 305; Indels 254; Gaps 44; Qy 66 YHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYY 114</dnj></him>	CIEIEÈEKKKKIEIEËEKKKKIEMËEEKNKIDDËKKNTYANDKIISHIDNVNCNIK 6 LAKVTDSSLKANATETL-AGLRNNLTLQIMDNNSIMAEAEK 777 : : : :	225 RRONSDNTSRTNWVPSVSNPGTTNTTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHV

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RESULT 21

$55101

$55101

Apporthetical protein YMR219w - yeast (Saccharomyces cerevisiae) hypothetical protein YM8261.13; hypothetical protein YM8261.13; hypothetical processeriate C;Species: Saccharomyces cerevisiae

C;Date: 08-Jul-1995 #sequence_revision 09-Mar-1996 #text_change 29-C;Accession: $55101; $57587

R;Dedman, K.; Brown, D.; Bowman, S. submitted to the EMBL Data Library, June 1995

A;Reference number: $55089

A;Accession: $55101

A;Molecule type: DNA

A;Residues: 1-711 <DED>
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                                                                                                                                                                                                                                                            HVPQICF -- LNEOLKEIR-YTRKLVDPQTQVTTTE
                                                                                                                                                                                                                                                                                    EVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEK
                                                                                                                                                                                                                                                                                                                                           DLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSE--DPNKNFKADEEPVEETPAEP
                                                                                                                                                                                                                                                                                                                                                                    EAAKIEAQLPLVPTVPEQIDGT----DPSLL-----
                                                                                                                                                                                                                                                                                                                                                                                               NRVKGEKRIPLV-RLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLE
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                                                                                                                                                                                                                                                                                                             ----FIVKTDQFEIVDPN----LDEHNVNLIYTE-
                                                                                            #text_change 29-Oct-1999
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                STDSPDNFQESNDNT---EFSSTKYKVRNSDLEDDESLKKELTKAEVVDKLDEEESEDSY
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A;Cross-references: EMBL:Z49809; NID:g854459; PII
A;Experimental source: strain AB972
R;Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, June 1995
A;Reference number: S57587
A;Accession: S57587
A;Accession: S57587
A;Rolecule type: DNÄ
A;Residues: 608-1658 <SKE>
A;Cross-references: EMBL:Z4939; NID:g887599; PII
A;Cross-references: EMBL:Z4939; NID:g887599; PII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                           NTGDENKNQSKNFPGVANSTDKSTEDNTDEKYFSAINYT---
                                                                                                                                                                                                                                                                                                                                             EVVISESVYSSTSYEDNTVAMPPQVEYTSPFMNDPFNS--
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AWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKD--HSEDPN
                                                                                           SAAAIYNRVKGEKRIPLVRLPYMVEHTV------EVKNGNLIIPHKD--HYHNIKF
                                                                                                                                                                                         IISDE--GDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGD
                                                                                                                                                                                                                                            LAALAPAFTKKDAEFVEAGVTKSCLTSTSGHTNIFHTSKETKQVSDLDESTENVTF-ENE
                                                                                                                                                                                                                                                                                       LAFLAP-ITHPE----RLGKPNSQIEYTEDEVRI-----AQLADKYTTSDGYIFDEHD
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                                                DIIETASNVEENLRYCEKDMNEAEMSSGDECVKQNDDGSKTQISF
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Pred. No. 1.
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RESULT 22
S61103
SEC16 protein - 1
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A;Residues: 1-2195 <HAL>
A;Cross-references: EMBL:U41849; NID:g1147608; PID:g1147609; MIPS:YPL085w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 k;Hail, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, submitted to the EMBL Data Library. August 1995
A;Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm. A;Reference number: 859677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEC16 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein LPF1w; protein YPL085w
C;Species: Saccharomyces cerevisiae
C;Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 06-Feb-1998
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R; Hall, J.; Ahmed,
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  TPAEPEVPQVETEKVEAQLKEAEVLLAKVT. 742
                                                           SMOTSTEKIAEOKFSFLENDDDLLDDDDSFLASSE----EEDTVPNTDNTTNLTSKPVEE
                                                                                                                 G-YTLEDLFATIKY-YVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEE
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                                                                                                                                                                                                                                                                                        --GQNDFTGKNIENESQKLMGEGNHK----LPLSAEADIIEPGKDIQDQAEDLFTQSSGD
                                                                                                                                                                                                                                                                                                                                                 HMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADV--KANPTGDSAAAIYNRVKGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERLGKPNSQIEYTEDEVR----IAQLADKYTTSDGYIFDE---HDIISDEGDAYVTP
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Pred. No. 2.8;
9; Mismatches 241
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A;Residues: 1-1495 <BEV's
A;Cross-references: EMBL:AL162873
A;Cross-references: cultivar C
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A;Accession: T48429
A;Status: preliminary
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  DHSEDPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKEAEVLLAKVTDS-SLKANATE 752
                                                              --RNLQ---
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                                                                                                                                                                                                                                                                                           LSPKTPRVLPWEPDPETEKIRLRHQEIGGKRNSEEWMLDYALRQAISTLAPSQKRKVSLL
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                                                                                                                 HYHNIKFAWFDDHTYKAPNGYTLEDLFATIKY--YVEHPDERPHSNDGWGNASEHVLGKK 693
                                                                                                                                                                                                                                  PPSPDA----DVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PITHPERLGKPNSQIEYTEDEVRIAQLADKYTTS--DGY----IFDEHDIISDEGD---
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                                                           EDLKESAKLDGVSKDLEEKQQCSSLW-----RILCKQ
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Qy 476	Db 328 SPTNSGEGNSSAYSVEFGNSETTAAEMKKIAADEKLAEIVMADPKRVKRILANRVSAARS 387
Db 704 RYABIQTRQYRAPEVILKSGFNETADIWSFACMVFELVTGDFLFNPQKGDRYDKNEEHLS	Qy 679NDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPE 718
Qy 460 RNSDFQALDKLLERLN	Db 290 APTGRHYRSVSMDSCFMGKLNFGDESSLKLPPSSSAKV 327
Db 644 IDSNNTMNDLGNNQNSHKVVYINTEDGEYCIRPYDPSVYYHEKSCYKICDLGNSLWIDES	QY 631 IPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHS 678
Qy 411 LESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKG	Db 248 GTKKTNGGSSSDSEGDSSASGNVKVALSSSSSGVKRRAGGDI 289
Db 584 QNKNQLEVNLPNNKYPNSNDVYKFFEKDINKFPIYCDMFNHLIHPBALRLHELYMKNKKN	OY 571 AYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLI 630
Qy 369 IDSNSSLVSQLVRKVGEGYVFEEKGIGRYVFAKDLFSETVKN	Db 206 AMDDVFTAYMNLDNIDVLNSFGGEDGKNGNENVEEMESSRGS 247
524 TRKPYHYNTYFLNNPEKYRDNKMNPYLHRLPNDCL	Oy 511 TEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQ 570
Qy 328 ARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLK	Db 197KGR
482 KQTKKKKNINEPPYVKHKLRPSN	451 HKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEY
276 KLPLSQRHVES	151 VTFGFSSMMSQNQKSPPLSSLERSISGEDTSDWSNLVKKEPR-EGFY
Cy 21 NISKIWWYSONWCITIN- INISKINSNINGASGNULTUSLINGER (: : : : : : : : :	Qy 397YVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEA 450
419ŇICN	348 QPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISR
Qy 171 FNASDIIEDTGDAYIVPHGDHYHYIFKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSD	Db 42HHHFRHPFTGAPPPPIPPISPYSQIPATLQPRHSRSMSQPSSFFSFDSLPPLNPS 96
Db 387NNISIKEKINDCHSPNENKNKDNHNQCEDNSI	Qy 306 VPHGDHYHF
Qy 119 DAAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYI	Db 7 TTDTNMMQRVNSSSGTSSSSIPKHNLHLNPALIRS 41
Db 330 VQIEKQSTLSKNKKNEKDSYININNSLTNDDQNLKREDIKFNDKAEGITKYDMLNIK	Qy 246 TTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVA 305
QY 63GDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYYYLK	es 125; Conservative 84; Mismatche
277 TOKNOKNIEYDOKCTSSKENIEDNVSFV	ry Mat t Loca
Qy 11 TVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSH	A; Map position: 2
Query Match 3.7%; Score 154.5; DB 2; Length 1338; Best Local Similarity 16.6%; Pred. No. 1.8; Matches 153; Conservative 122; Mismatches 287; Indels 357; Gaps	A;Residues: 1-519 - KSTO> A;Residues: 1-519 - KSTO> A;Cross-references: GB:AE002093; NID:g4582442; PIDN:AAD24827.1; GSPDB:GN00139 C;Genetics:
C;Genetics: A;Map position: 3 A;Note: C0105w	420; MUID:20083487;
A;Residues: 1-1338 <law> A;Cross-references: EMBL:Z97348; NID:e1323671; PID:e1323672; PIDN:CAB10568</law>	
д н	H.; Moffat, Nierman, W
the EMBL Data Library, number: Z18934	: 02-Feb-2001 # ssion: G84598
S.: Barrell. B.	robable bZIP transcription factor [imported] - Arabidopsis thaliana ;Species: Arabidopsis thaliana (mouse-ear cress)
T18416 Typothetical protein C0105w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Spate: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 09-Jun-2000	ESULT 24
RESULT 25	Db 1439 EAEKVN 1444
Db 447 RDALSEKLNEBVQKLKLVIGEPNRRQSGSSSSESKWSLN 485	Qy 791 SKEKIN 796
758 RNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSVSKEKIN	1379 NINNEETROKSETLOVSKVRIDRWSNIKRAIILRRFVKALENVRKFNPREPRFLPPNPEV
Db 388 KERKTRYMAELE-HKVQTLQTEATTLSAQLTHLQRDSMGLTNQNSELKFRLQAMEQQAQL	Qy 753 TLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSV 790
719	Db 1319 MEDNEKNQTLPEETRKEEEEEELKEDTSVDGEKMELYQTEAVELLGEVIDGISLEESQDQ 1378

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ASS surface protein - Staphylococcus saprophyticus
C;Species: Staphylococcus saprophyticus
C;Species: Staphylococcus saprophyticus
C;Accession: T30290
R;Hell, W.; Meyer, H.G.W.; Gatermann, S.G.
Mol. Microbiol. 29, 871-881, 1998
A;Title: Cloning of aas, a gene encoding a Staphylococcus saprophyticus surf
A;Reference number: Z20809; MUID:98389318; PMID:9723925
A;Accession: T30290
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1463 <HELP
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Best Local
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130; Conserv
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                                                                                                           HYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKID
                                                                                                                                               VNQDDTHSDANASDDVK------DQNESETQN---DKAETSNEDDVASSDVKQDD
                                                                                                                                                                                    SWNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSR-TARGVAVPHGD
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-QNESATQDDKA---TSKED
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C;Bpecies: Plasmodium falciparum
C;Bpecies: Plasmodium falciparum
C;Bpecies: Plasmodium falciparum
C;Bcecies: Plasmodium falciparum
C;Accession: E71619
R;Gardner, M.J; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
A;Reference number: A71660; MUID:99021743; PMID:9804551
A;Reference number: A71660; MUID:99021743; PMID:9804551
A;Recession: E71619
A;Recession: E71619
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A; Residues: 1-1516 <GAR>
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                                                                                                                                                                                                                                                                                                                                                                                                              DGKQAT----OKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDA 77
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                                                                                                                                                                                                                                                              ---QKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDH 191
                                                                                                                                                                                                                                                                                                                                                                               DGDMGTVENINKLDNRNKDENNLSYSINYN----KVQD----VNNNND
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 ITNDEKSININNYNNNNNNNNNNNNNNDNNDVIIEHNKNNMNIYDNKYNVECSSEKIN 546
                                    -TNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDI-----DSLLKQLYKLPLSQRHVE 285
                                                                                                                                                                                                                           DDDDEKEDIQNKNG-----
                                                                                                                                               YESIPKTFKGFLCMRRPVDIIDISNYNTEMLEISETLKVHENKFKQHLNVLDENNSTPVV 430
                                                                                                                                                                                        YHYIPKN----ELSAS---
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                                                                                                            -ELAAAEAFLSGRGNLSN-----SRTYRRQNSDNTSR-----
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A;Status: preliminary
A;Molecule type: mRNA
A;Residus: 1-1443,3585-3924 <OTT>
A;Cross-references: EMBL:X56958
A;Cross-references: EMBL:X56958
A;Cross-references: EMBL:X56958
                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-3924 <CHA>
A;Residues: 1-3924 <CHA>
A;Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288
R;Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.
J. Cell Biol. 114, 241-253, 1991
J. Cell Biol. 114, 241-253, 1991
A;Title: Isolation and characterization of cDNAs encoding human brain anky.
A;Reference number: A39643; MUID:91302466; PMID:1830053
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C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 13-Aug-1999
C;Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ankyrin 2, neuronal long splice form - human
N;Alternate names: ankyrin B, 440K splice form; ankyrin-B;
N;Contains: ankyrin 2, short form
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A;Status: prelimina
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A;Status: prelimina
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                                                                                                                                    Cross-references: GB:X56957
                                                                                                                                                         Residues:
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              Sahr,
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R;Chan, W.; Kordeli, E.; Bennett, V.

Cell Biol. 123, 1463-1473, 1993
A;Title: 440-kD ankyrinB: structure of the major developmentally regulated domain A;Reference number: A49462; MUID:94075409; PMID:8253844
A;Accession: A49462
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A;Accession: A40334
A;Molecule type: DNA
A;Residues: 463-474, 'PE', 447-495 <TSE>
A;Cross-references: GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648
R;Chan, W.; Kordeli, E.; Bennett, V.
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C; Superfamily: ankyrin;
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A;Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;694-726/Domain:
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R;Zhao, Y; Kappes, B.; Yang, J.; Franklin, R.M.
Eur. J. Biochem. 207, 305-313, 1992
A;Title: Molecular cloning, stage-specific expression and A;Reference number: $23466; MUID:92331669; PMID:1378403
A;Accession: $23467
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-749 <ZHA>
A;Cross-references: EMBL:X63648; NID:g9937; PID:g9939
C;Superfamily: human long-chain-fatty-acid-CoA ligase; accC;Keyword8: acid-thiol ligase; coenzyme A
F;103-732/Domain: acetate-CoA ligase homology <ACL>
                                                                                                                                                                                                                                                                                                                                                                                                                              probable long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) - malaria parasite (C;Species: Plasmodium falciparum C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 03-Jun-2002 C;Accession: S23467
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18.7%; Pred. No. 0.84;
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A36685
                                                                                                                                                                                                                                                                                     A;Gene: FlyBase:Map205
A;Cross-references: FlyBase:FBgn0002645
C;Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1163 <IRM>
A;Cross-references: GB:X54061; NID:g8201;
C;Genetics:
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                               RTYRRQNSDNTSRTNW------VPSVSNPGTTNTNTSNNSNTNS----QASQSND 266
                                                                                                          NASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAE-----AFLSGRGNLSNS
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                                                                         --SDEVDGEED
                                                                                                                                              HEDNAQLDNYLQNRLAESLQICGGAGEHNPHLADATGGNGCAPGIAPSK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPLVRLPYMVEHTVEVKNGNLIIPHKDHY-HNIKFAWFDDHTYKAPNGYTLEDLFATIKY 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSLSDKE----KVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNR---VKG--
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----DSDNQVHGNGAAAVFNLYEEDVEVIKNDGDFSTNSNTTTSTDEVVARQAQEPNQ 149
                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                               3.6%; Scc
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                                                                         -EEWKYI--HEVRQSEKLQQEKLPLTKETGNGFGPGR-----
                                                                                                                                                                                                                 Score 151.5; D
Pred. No. 2.2;
05; Mismatches
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A;Molecule type: DNA
A;Residues: 643-1008,'AVSPMEM',1016-1017,'SRTRI'
A;Cross-references: EMBL:M88606; NID:g172077; PII
                                                                                                                                                submitted to the EMBL Data A; Reference number: S27437 A; Accession: S27437
                                                                                                                                                                                                            A;AGCEBBALLA.
A;ANOlecule type: DNA
A;Residues: 1-1176 <ALE>
A;Cross_references: EMBL:Z74820; NID:g1419910;
A;Cross_reference: strain S288C
                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein YOL078w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O1110
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text_change
C;Accession: S66771; S27437
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submitted to the Protein Sequence
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                                       A; Map position:
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                                                          SGD:S0005438
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ribonuclease E XF2607 [imported] - Xylella fastidiosa (strain 9a5c)
c;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: B82538
C;Accession: B82538
Consortium of the Organization for Nucleotide Sequence and Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
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                                                                                                                                                                                                                                       IN 796
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.8; Mismatches
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DAD-VKANPTG

593 754 552 716 498

1004

892

952 739 851 653 811

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A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Abrines, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Faccincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigi J.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigi Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, F.A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D., F.G.; Nunes, L.R.; Oliveira, M.A.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasai A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvein, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
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A;Note: for a complete list
A;Accession: B82538
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C;Superfamily:
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A;Contents: annotation
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A; Residues: 1-1132 <SIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELLMKDP----NYKLKDE-DIVNEVKGGY----VIKVDGKYYVYLKDAAHADNVRTKE-E
AHSNTTRHTSGRRLETLSTAHTPAKASPSEHITPTSRSNANAKTTKTEIPNKPTNANSDT
                                            GHS----HWIGK-
                                                                                           TAPQSMMETTSRTHVASQMAPQSETSAASTTSHTSVQATTTHTHKDVVSDSPSR--TPYK
                                                                                                                                          -KPNSQIEYTEDEVRIAQLADKYTTSDG---
                                                                                                                                                                                                                                                                                                                                 DFQALDKLLERLNDEST------
                                                                                                                                                                                                                                                                                                                                                                                ----LTAEAVLTNMPAPSMTATPSGKDQNALPTTSNVTQDTSNALIEAQSTTKTNIDTNT
                                                                                                                                                                                                                                                                                                                                                                                                                             SETVKNLESKLSKQESVSHTLT--AKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPRQPQPQLPKTPRTQSQPTQN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNTDKRQTASNSSHPAPLQQNRNGNVQRNERNHRDGRIATSNTQPQQQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDN-----TSRTNWVPSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVLVQTPVEIANYLLNEKRRAINEIEKRHDAPIIIIADEQLH----TPHYEVTRLRENE
                                                                                                                                                                                       TETDNADNI EAPQALRPAMQENKRQPEFEFDDLAPAAPI TAPLRKAI AAEREEI SADLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --SNPGTTNTNTSN-----NSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 104;
                                                                                                                                                                                                                                                                                  -QQNNHEGTANNDGSNRRRRGRRGGRRRRRNTSLGNETNAVSESNSIKLSND
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Pred. No. 2
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ed. No. 2.5;
Mismatches 280;
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                                          ----DSLSDKEKVAAQAYTKEKGI---LPPSPDADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -STKTTLDKQPAPVLYGEDNTLQK---AKPIP
                                                                                                                                        ----YIFDEHDIISDEGDAYVTPHM
                                                                                                                                                                                                                                        -LAFLAPITHPERLG--
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rhoptry protein - Plasmodium yoelii (fragment)
(,Species: Plasmodium yoelii
(,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_
(,Accession: T28676, A45521
(,Accession: T28676, A45521
R,Sinha, K.A.; Keen, J.K.; Ogun, S.A.; Holder, A.A.
Mol. Biochem. Parasitol. 76, 329-332, 1996
A,Title: Comparison of two members of a multigene family
A,Reference number: Z20507; MUID:97077455; PMID:8920022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-2401 <SIN
A;Residues: 1-2401 <SIN
A;Residues: 1-2401 <SIN
A;Cross-references: EMBL:U36927; NID:g1041784; PID:g1041785; PIDN:AAB41263.1
A;Cross-references: EMBL:U36927; NID:g1041784; PID:g1041785; A.
Mol. Biochem. Parasicol. 42, 241-246, 1990
A;Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple A;Reference number: A45521; MUID:91101660; PMID:2270106
A;Accession: A45521
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A;Molecule type: DNA
A;Residues: 2260-2401 <KEE>
A;Cross-references: GB:M34281
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KIKKIIDKVKEY-TDEIEKNNKKINAELSNSEKIITQLKENSSLKE-----CQSKIKST
                                                                                                                                                                                                                                                                                                                                                                                YVIKVDGKYYVYLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KANPTGDSAAAIYNRVKGEKRIPLVRLPYMV---EHTVEVKNGNLIIPHKDHYHNIKFAW
                                                                     LFEKYEQEVTVLLNKYYAVELKNK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TESETTQPPVRKPRLPMQNPLPKVVAPLED.
                                                                                                                                                          NFNNIEMADTKSQYILNIKKNNGTNNTDYNIKELKEHKKKSNVYKDEAGKNTQEIKKNKE 1146
                                                                                                                                                                                                   TYRRQNSDNTSRTNWVPSVSNPGTTNTNTS-----
                                                                                                                                                                                                                                                                                        TDDGYIFNASDIIEDTGD--AYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AYIDDLDNIKKKS----QEIEKEMNINMDIKMDIHKEMKALNISHDDYKIYHTTSKNHEE
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                                                                                                            -DIDSLLKQLYKLPLSQRHVESDGLVFDPAQITS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 150; DB Pred. No. 7.6;
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                                                                     FDKTKNYSEQIIKEIKDAHNTFTSQADK 1198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -PNYKLKDEDIVNEVKGG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coding
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GRYTTDDGYIFNASDII 177

309

260

-EPF

-PEPSPGPQ

573 362 526

468

408 235 355

283

319

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A;Note: clone PTPZEI
A;Note: clone PTPZEI
C;Genetics: <PTPZEI
C;Genetics: <PTPZEI
C;Genetics: <PTPZEI
C;Genetics: <PTPZEI
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
F;25-304/Domain: protein 4.1 membrane-binding domain homology <B41>
F;25-304/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1109/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1115/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein-tyrosine-phosphatase (EC 3.1.3.48) 2E - rat C:Species: Rattus norvegicus (Norway rat) C:Species: Rattus norvegicus (Norway rat) C:Accession: S:196 #sequence revision 03-May-1996 #text_change 22-Jun-1999 C:Accession: S51005; S51161 C:Accession: S:1005; S51161 R:L'Abbe, D.; Banville, D.; Tong, Y.; Stocco, R.; Masson, S.; Ma, S.; Fantus FEBS Lett. 356, 351-356, 1994 A:Title: Identification of a novel protein tyrosine phosphatase with sequence A:Title: Identification of a novel protein tyrosine phosphatase with sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 34
S51005
                                                                                                                                                                                                                                                          A;Cross-references:
A;Genetics: PTP2E1
C;Genetics: <PTP2E>
                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 840-1175 < LAB>
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A;Genetics: PTP2E
A;Accession: S51161
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A; Residues: 1-1175 < LAA>
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      Conservative
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                    3.6%;
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      87;
  Score 149.5; I
Pred. No. 2.9;
B7; Mismatches
                                                                                                                                                                                                                                                                                                      NID:g603228;
                                                                                                                                                                                                                                                                                                                                                                                                         NID:g662113;
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                       9
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  273;
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  213;
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  30;
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                                                                                                                                   R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 125-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; pMID:11418146
A;Accession: A89959
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1274 <KUR>
                                                                                                                                                                                                                                                                                                                                        hypothetical protein SA1562 [imported] - Staphyloco
;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001
C;Accession: A89959
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                                                            A;Gene:
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  Query Match
Best Local
                                                                                                    Cross-references: GB:BA000018; PID:g13701536; Experimental source: strain N315
  Local Similarity
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  Score
Pred.
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  149;
No. 3
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. 4;
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                                                                                                                     PIDN:BAB42830.1; GSPDB:GN00149
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                    Length 1274;
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(strain 22-Oct-2001

N315

Oguc

833 605 -THQPRRH

AFLAP

494 691

751

554

451

Gaps

42

144 1772

1832

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RESULT 36
A42771
reticulocyte-binding protein 1 - Plasmodium vivax c;Species: Plasmodium vivax C;Species: Plasmodium vivax C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 C;Accession: A42771
R;Galinski, M.R.; Medina, C.C.; Ingravallo, P.; Bar Cell 69, 1213-1226, 1992
                                                                                                                            Cell 69, 1213-1226, 1992

A;Title: A reticulocyte-binding protein complex of Plasmodium vivax merozoites. A;Reference number: A42771; MUID:92315338; PMID:1617731

A;Accession: A42771
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                                    A;Molecule type: DNA
A;ResidueB: 1-2829 <GAL>
A;ResidueB: 1-2829 <GAL>
A;Rserimental source: Belem strain, merozoites
A;Note: sequence extracted from NCBI backbone (NCBIN:108114, NCBIP:108115)
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                                                                                           EKLL
                                                                                                                                  ENVKKKESILNDLYEQERLL-KIGEHLDEIKRNVTETLSSYEIDQKMEMMSKN-LLEKK 2515
                                                                                                                                                                                                      ---MEVNTETIHRVNDYIEKITNKLVQAKTEYEQILENIKQNDDMLQNIFLKKVSIIEYF
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                                                                                                                                                                                                                                                                                                                                                      PMIELHKGMNETNNKSLLEKEKKLKSVNDHMHSMEAEMIKNGLKYTPESVQNINNIYSVI 2347
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                                                                                                                                                                  EVPQVETEKVEAQLKEAEVILAKVTD--SSLKANATETLAGLRNNLTLQIMDNNSIMAEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ES---KHADYRR--DANSMYESMVTLANYFLSDEAKISSGMEFNAEMKSNFKTDLELEIF 1947
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                                                                                             779
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submitted to Ge A;Description: A;Accession: F8 A;Status: preli A;Accession: F8 A;Status: preli A;Accession: F8 A;Cess-referen A;Access-referen A;Cross-referen A;Cross-referen C;Gene: UU482 A;Genetics: A;Genetics: A;Genet U482 A;Genet U482 A;Genet 5048 A;Cross-referen Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code: Code	TREE TO SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE TH

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8	LKANATETLAGLRNNLTLQIMDNN
Db	1335 AVTLIKGQRNYQFEFSNLIKNRLYTFSKIVYETNNQTLHKLDTLTHQFSINPSNNAVSLK
9	775 AEKILALIKGSNPSSVSKEKI 795
рb	1395 NNTNIEITKRILVNNDQSLISAKI 1418
RESULT 38 B89921 hypothetical hypothetical C;Species: S C;Date: 10-M C;Accession:	ESULT 38 89921 ypothetical protein ebhA [imported] - Staphylococcus aureus (strain N315); Species: Staphylococcus aureus ;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001; Accession: B8927
R;Kuroda, ma, A.; M C.; Shib	; Ohta, T. tani-Ui, Y T.; Hattor:
A;Title A;Refer A;Acces A;Statt	A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Accession: B89921 A;Accession: B89921 A;Status: preliminary
A;Resic A;Cross A;Exper C;Genet A;Gene	A;Residues: 1-6713 <kur> A;Cross-references: GB:BA000018; PID:g13701232; PIDN:BAB42527.1; GSPDB:GN0014 A;Experimental source: strain N315 C;GenetLcs: A;Genet cs:</kur>
Query M Best Lo Matches	y Match Local Similarity 18.5%; Pred. No. 38; hes 170; Conservative 127; Mismatches 373; Indels 250; Gaps
8	16 NRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYN
Ф	3 NLQTAINDKSGTLASQNFLDADEQKKNAYNQAISAAETILNKQTG
80	71 GKVPYDAIISEELLMKDDNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAA
рb	48PNTAKTAVEQALNNVNSAKHALNGTQNLNNAKQAAITAINGASDLNQKQKDALKAQA
40	TPRN
В	105 NGAQRVSNANDVQRNATELNTAMGQLQHAIADKTNTLASSKYVNADSTKQNAYTT
9	166 DDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASEL-AAAEAFLSGRGNLSNSRTY
Дb	160 KVTNAEHIISGTPTVVTTPSEVTAAANQVNSAKQELNGDERL
8	225 RRQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQR
Дb	202 RVAKQNANTAIDALTQLNTPQKAKLKEQVGQANRLEDV
Qy	283 HVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHW
DЬ	241 SVQTNGQSLNNAMKGLRDSIANETTVKASQNYTDASPNNQSTYNSAVSNAKGIINQTNNP
Qy	341 VPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVG
Дъ	301 TMDTSAITQATTQVNNAKNGLNGAENLRNAQNTAKQNLNTLSHLTNNQKSAISSQIDRAG
Qy	385 EGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYD

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R;Harris, B.
submitted to the EMBL Data Library,
A;Reference number: Z19441
A;Accession: T21558
A;Accession: T21578
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T21558
T21558
hypothetical protein F29G6.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T21558
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:Z78543; PIDN:CAB01754.1; GSPDB:GN00028; CESP:F29G6.3b
A;Experimental source: clone F29G6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-1785 <WIL>
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Best Local Similarity
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ASDIIEDTGDAYIVPH--GDH----YHYIP-KNE--LSASEL---
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                                                                                                                                                                                                                                                                                             126;
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Pred. No. 5.9
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Ack, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AG1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein 1mc0086 [imported] - Listeria monocytogenes (strain EGD-C;Species: Listeria monocytogenes C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AG1085 C;Accession: AG1085 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.
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AG1085
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A; Residues: 1-1959 <GLA>
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                                                               18
                                                                                                                                             Similarity 17.7
54; Conservative
                     --YVYLKD--
                                                               AIVSAFFLMRDDAYAIETEGFTYSPKGKVVDFSSEAKYNDTWINNEKTITDKKEMKPINL
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                                                                                                      AIISEELLMKDPNYKLKDEDIVNEVKGGYV-IKVDGKY--
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                                                                                                                                               125;
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Pred. No. 6.8;
  AAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALA 157
                                                                                                                                               Mismatches
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Voss, H.; Wehland,
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RESULT 41 T38495 T38495 hypothetical protein SPAC29B12.07 - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T38495 R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, September 1997 A;Accession: T38495 A;Accession: T38495 A;Accession: T38495 A;Accession: T38495 A;Molecule type: DNA A;Molecule type: DNA A;Accession: 1-1969 <gen> A;Cross-references: EMBL:Z99164; PIDN:CAB16252.1; GSPDB:GN00066; SPDB:SPAC29B12.07</gen>	754 LAGLRNNLTLQIMDNNSIMAEAEKLLA 780 		QY 673 DERPHSNDGWGNASEHVLGKKD	Qy 642 FAWFDDHTYKAPNGYTL	QY 584DADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIK 641	Qy 541 EGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSP 583 : ::	Qy 503 KPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD 540	Qy 462 SDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLG 502	Qy 408 VKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNILTEAHKALFXNKGRN 461	Qy 361 PQPAPNLKIDSNSSLVSQLVRKVGEG	Qy 301 ARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPG 360	Oy 241 VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT 300	Qy 182 -DAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS 240	Db 78 ARTLFLKDGRIQFIGKSVAVKSASDLIELPSKTSITESKGSYKAKSDSNKTLA 130 Qy 158 RSQGRY-TTDDGYIFNASDIIEDTG- 181 ;
Qy 632 PHKDHYHNIKFAMFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEH 688 1	587 VKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLII	553SHWIG-KDSLSDKEKVAAQAYTKEKGTLPP-SPDAD	Qy 508 IEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGH 552	Qy 448 TEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKDNSQ 507 : ::	Qy 413 SKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLL 447	Qy 364 APNIKIDSNSSLVSQLVRKVGEGYVFEEKGISRVVFAKDLPSETVKNLE 412	Qy 304 VAVPHGDHYHFIDYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQP 363	Qy 244 PGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARG 303 :-	Qy 189GDHYHYIPKNELSASELAAAEAFLGGRGNLSNSRTYRRQNSDNTS-RTNWVPSVSN 243	Qy 134 RQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPH- 188	Qy 74 PYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHADNVRTKEEIN 133	Qy 14 ENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYNGKV 73. :	Query Match 3.6%; Score 148.5; DB 2; Length 1969; Best Local Similarity 19.6%; Pred. No. 6.8; Matches 179; Conservative 113; Mismatches 288; Indels 331; Gaps 46;	A;Experimental source: strain 972h-; cosmid c29B12 C;Genetics: A;Gene: SPDB:SPAC29B12.07 A;Map position: 1 A;Introns: 664/2

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hypothetical protein PFB0765w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: E71606
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin,
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith,
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
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C;Superfamily: h
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                                                                                                                                                           IYNRVKGEKRIPLVRLPYMV-EHTVEVKNG----NLIIPHKDHYHNIKFAWFDDHTYKAP
                                                                                                                                                                                                                                  SDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAA
                                                                                                                                                                                                                                                                       IKNLEDDLL-
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                                                     NKYDKEINMI IEQYNKKI QEEKDMLNNKI KSMDQTHKNQI EEMQEENKKELKRLKNVCDM
                                                                                       NGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKN-----
                                                                                                                            --EFLKEEEKKKNIDMVYKIKEYEIQIKEKENEIDSLKKNEQNLHVLKNEELNEKEIILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KQNYYYLKKEYDLKNKELEKNIEHGKKLEHELSHC-----
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-----EKKKCIENLKDELINIKKKMEDKM-----HMTNEMDLL
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T2245B
hypothetical protein F49E2.5a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te)
C;Accession: T2245B
R;Sulston, J.
Submitted to the EMBL Data Library, October 1994
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A; Introns: 37/2;
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A; Accession: T22458
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Best Local Similarity
Matches 177; Conserv
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                                                                                                                                                                                                                                                                                                          --LEERIARIIPLRYRSNHWVP-----
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                                                       PVQAAPTSKKPTADDSMDFLDFVTAKEERVEEVAPVQEQVKEQKNESPESEPVAKLITVS
                                                                                                                            DDSMDFLDFVTAKPDRSEVAAPVEVAKVDESTAVTSENRKKNKKDKKKSESEKAVE---E
                                                                                                                                                          SHTL-----TAK----KENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLE
                                                                                                                                                                                                                                  KIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKD-LPSETVKNLESKL-----SKQESV 421
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                                                                                         RLNDESTNKEKLVDDLLAFLAPIT----HPERLGKPNSQIEYTEDEVRIAQLADKYTT--
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                                                                                                                                                                                               -VEQVVETTPPASENKKKN-----KKDKKKSESEKAVEEPVQAAPSSKKPTA 451
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1%; Pred. No. 3.7;
123; Mismatches 351;
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Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morri A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

**Bafarance number: A95000; MUID:21357209; PMID:11463916
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R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heion, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-1856 <KUR>
A;Cross references: GB:AE005672; PIDN:AAK74260.1;
A;Experimental source: strain TIGR4
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C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: C95008
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                                                                                                                                                                             SGRGNLSNSRTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPAYTEPLATKGTQEPGHEGKATVREETLEYTEPVATKGTQEPEHEGEAAVEEELPALEV
                                RIARIIPLR-----YRSNHWVPDSRPEQPSP---QPTPEPSPGPQPA-----PNLKI
                                                                      PEYKLPLETKGTQEPGHEGEAAVREDLPVYTKPLETKGTQGPGHE-
                                                                                                        QLYKLPLSQRHVESDGLVFD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGSKKNKKNKKNSESESAPAAEPVKEVTPEIVEEVFEKKTVTPSTEAAAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEPKKVEKPVAPVSKKPTADDNMDFLDFVTAKPEKTESVEEHIEAPMIVEPVHAENETAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNTLSPSQHSTPSPNSVLLNGPQSKSSKRKHHHKKNKKRTDSEMSQEPSKEDLEFLEFLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVA-VSKKPTADSMDFLDFVTPKTEAESTSEAPAPVVSKPTESIEDLEIVTYEHVADV-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDADVKANPTGDS-----AAAIYNRVKGEKRIPLVRLP-----YMVEHTVEVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus sanguis IgA-specific metalloendopeptidase
                                                                                                                                                                                                                                                                                                                                                                  Conservative 109; Mismatches 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSV 790
                                                                                                                                                                                                                                                                                                                                                                                   3.6%; Score 148; DB
19.8%; Pred. No. 6.7;
                                                                                                        ----PAQITSRTARGVAVPHGDHYHFIPYSQMSELEE
                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----QDPVSAKQEVLPEHVPSE---IPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --NASEHVL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID:g14971537; GSPDB:GN00164; TIGR:SP4
                                                                                                                                                                                                                                                                                                                                                                                                  Length 1856;
                                                                                                                                                                                                                   -LSEKSSIAADNLSSNDSFA
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                  242;
                                                                      -GEAAVREE
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                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                             307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Morrison
                                                                                                                                                                                                                                                                                                                                                                                                                                   transfer complex protein TrsI - Staphylococcus aureus C;Species: Staphylococcus aureus C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change C;Accession: A56976 R;Morton, T.M.; Eaton, D.M.; Johnston, J.L.; Archer, G.L. J. Bacteriol. 175, 4416-4447, 1993 A;Title: DNA sequence and units of transcription of the conjugat A;Reference number: A36891; MUID:93322322; PMID:7687249 A;Accession: A56976
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A56976
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C;Superfamily: DNA topoisomerase I topA
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                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-700 < MOR>
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                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                    Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               632
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                                                                                                                                                                                                388 VFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAY-NL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            626
                 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YFVKVK----
                                                                                                                                                            IFKENKIDEVIIATD-PAREGENIAYKILNOLKVTDKVTIKRLWLTSKVESSIRKAFKNI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMAEAEKLLALLKGSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPQVETEKVEAQLKEAEVLLAKVTDSSL-----KANATETLAGLRNNLTLQIMDNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTRNRTEIONIPYTTEEIODPTLLKNRRKIEROGOAGTRTIQYEDYIVNGNVVETKEVSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSNSSLVSQLV-
               NMVYNRENNIKGFKGKKFYKVSATINKDEQEVK-TELKNKFDSEDELHEFLF-ENDITDL
                                                                                     LPKEKTYGFYKEGRARELSDWLVGINLSRHFTKISRE-
                                                                                                                        LTEAHKALFXNKGRNSDFQ-----ALDKLLERLNDESTNKEKLVDDLLAFLAPITHP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTG---KLIANHQDSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRDLDIKTVSADSKENVAALAKAANSANINNVAVEGKISGAKSVAGLVASATNTVIENSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DM-----TADEVSLGDKQTSYLTGAFTGSLIGSDGTKSYAIYDLKKPLFDTLNGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DERPHSNDGWGNASEHVLGKKDHS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDQLVEEGTDGYK-----DDYTFTVAKSKAEQPGVYTSFKQLVTAMQSNLSGVYTLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHT-----VEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TETSTQDFQL--EYKKIEIKDIDSVELYGKENDRY-----RRYL---SLSEAPTDTAK 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----AKTOVFHG-DKLVKEVDIENPAKEOVISG-LDYYTPYTVKTHLTYNLGENNE--EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPI --- TH-PERLGKPNSQIEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEVA---PVNEVVKVGTLVKVKPTVEITNLTKVEN----KKSITVSYNLIDTTSAYVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLL--TEAHKAL
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                   3.5%;
                                                 ---ERLGKPNSQIEYTEDEVRIAQLADKYTTSD----GYIFDEHDIIS- 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   786
                                                                                                                                                                                                                                  84;
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                                                                                                                                                                                                                                                 Score 147;
Pred. No. 1
                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                              PIDN:AAA71960.1; PID:g310616
                                                                                                                                                                                                                                                 .8;
                                                                                                                                                                                                                                    174;
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                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                     Length 700;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conjugative
                                                                                   -LGNDGVIHIGRVSSPTL
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                                                                                                                                                                                                                                    134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transfer gene
                                                                                                                                                                                                                                  Gaps
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 46
F84730
                                                                                                                                                                                                                                                                                                                                                                                                                                          문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable myosin heavy chain [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: F84730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE002093; NID:g6598483; PIDN:AAC69932.2; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-1269 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Gene: At2g32240
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Best Local
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268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160;
                                                                                                                                                                                                                                                                                                                                                        72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 NGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHADNV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----NTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVES 286
                                                                                                                                                                                                                                                                                                                                                                                               RTKEEINR------QKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLKAMANPIETLEDEGLKSTLKEVKGLGTPATRADIIENLKKNKYIQVQKNKIYITKNGI
                                                                                      ESQKALEFSELLKSTKESAK---
                                                                                                                                                                           GIELESSRKKLI-----SASHADS
                                                                                                                                                                                                                                                                  LEETEKKHGDLEVVQKKQQEKIVEGEERHSSQLKSLEDALQSHDAKDKELTEVKEAFDAL
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EKMSENEKVEAALKSSAGELAAVQEELALSKSRLLETEQKVSSTEALIDELTQELEQKKA 327
                                         DSRPEQPSPQPTPEPSPGPQPA------PNLKIDSNSSLVSQLVRKVGEGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                          NGEVP-----KEE---KEEEDGEFIKVEKEAFDAKDDAEKADHVPVE
                                                                                                                             D---GLVF-DPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVP
                                                                                                                                                                                                                                                                                                        IEDT----GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSD--
                                                                                                                                                                                                                                                                                                                                                    EQKEVIERSSSGSQRELHESQEKAKELELELERVAGELKRYESENTHLKDE--LLSAKEK
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A; Introns: 10/1; 43/3; 61/3; 88/3; 110/3; 144/2; 183/3; 218/3; 252/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library
A;Reference number: 219441
A;Accession: 721559
A;Status; preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F29G6.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
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A; Residues: 1-1929 <WIL>
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17.6%; Pred. No. 8;
tive 125; Mismatches
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A;Residues: 1-2004 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75263.
A;Experimental source: strain TIGR4
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                A;Gene: SP1154
C;Superfamily:
                                           A; Experimental C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                      PEVPQVETEKVEAQ
                                                                                                                                                                                                                                                                                                                                                                                                           --VEHPDERPHS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADK
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                Streptococcus
                 sanguis
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                 IgA-specific
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                metalloendopeptidase
                                                                 PID:g14972632;
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                                                                                                                                                                                             T.D.; Peterson, S.; Hei
Radune, D.; Holtzapple,
                                                                 GSPDB:GN00164;
                                                                                                                                                                                                                                                              (strain TIGR4)
                                                                                                                                                         В.А.;
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                                                                                                                                                           Morrison
                                                                   TIGR:SP
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hypothetical protein YOR195w - yeast (Saccharomyces W,Alternate names: hypothetical protein O4806 C,Species: Saccharomyces cerevisiae C,Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #c,Accession: S67087 R,Hughes, B.; Pohl, T.M.
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Best Local Sim
Matches 173;
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GTP--RNDGAVALARSQ------GRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHY
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LPFYNKATIVKYGNLVNENSLLYQKELLSAVMMKDN
                                                                                                           GTMLDASQIASKKAEINPLILPTVEPLSTSGK-KDSD--FSKVAYYQAKRNLTYKNIEKL
                                                                                                                                                               NFKADEEPVEETPAEPE----VPQVETEKVEAQLKEAEVLLAKVTDSSLKANAT---
                                                                                                                                                                                                                          VK--DTFSSKANRVYNV----TL--
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                                                    AGLRNNLTL----QIMDNNSIMAEAEKLLALLKGSN
                                                                                                                                                                                                                                                                           FAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNK 701
                                                                                                                                                                                                                                                                                                                                                                                       ----SAAAIYNRVKGEKRIPLVRLPYMVEHT-----VEVKNGNLIIPHKDHYHNIK
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5; Mismatches
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#text_change 19-Apr-2002

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submitted to the Protein Sequence Database, July 1996
A;Reference number: S66685
A;Accession: S67087
A;Molecule type: DNA
A;Residues: 1-821 <HUG>
A;Cross-references: EMBL:Z75103; NID:g1420464; PID:e252389; PID:g1420465; GSPDB:GN00015;
A;Kyperimental source: strain S288C
C;Genetics:
RESULT 50
$3,4032
kinesin-related protein cut7 - fission yeast kinesin-related protein cut7 - fission yeast C;Species: Schizosaccharomyces pombe C;Date: 13-Jan-1995 #sequence_revision 13-Jan C;Accession: S14032
R;Hagan, I; Yanagida, M.
Nature 347, 563-566, 1990
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A;Cross-references: SGD:S0005721
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Map position: 15R
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                                                                                                                                                                                              KMWQSKYETVEDEAKIRNAEVTELNGDIEDLKESKLHLEETITELENKVHKLENECELEK
                                                                                                                                                                                                                        ----PQVETEKVEAQLKEAEV--LLAKVTD-SSLKANATETLAGLRNNL------
                                                                                                                                                                                                                                                    NNLQQKMDDLNNLNDDNLKVVQDKLIKNEETLKLKEAEIDSLNSEMDELKKQITSKDDEF
                                                                                                                                                                                                                                                                            DERPHSNDGWGNASEHVLG-------KKDHSEDPNKNFKADEEPVEETPAEPEV
                                                                                                                                                                                                                                                                                                         LNDKIEST-----DIVLKSKENELDNLKLSL--KETLSISKDFNDSDLIGQINELISTK
                                                                                                                                                                                                                                                                                                                                    LPYMVEHTVEVKNGNLIIPHKDH-YHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHP
                                                                                                                                                                                                                                                                                                                                                              HENTVNTLQQNEKI - - - - - LNDKNVELENMKAELKGN - - - NDKLSEYETTLNDLNSRIVQ
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ilarity 19.2%;
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                                        _revision 13-Jan-1995
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  - ADILHSHLNDTNSNIRKANEIMNNRSEEFLRNAASQAEIVGANKERIQKTVE - -
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A;Title: Novel potential mitotic motor protein encoded by the A;Reference number: S14032; MUID:91015362; PMID:2145514
A;Accession: S14032
A;Molecule type: DNA
A;Residues: 1-1073 <+HAG>
A;Cross-references: EMBL:X57513
A;Note: the authors translated the codon GCC for residue 2 as C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: probably involved in mitotic spindle body duplication (C;Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology C;Keywords: ATP; microtubule binding; mitosis; nucleotide binding; P-loop F;61-415/Domain: kinesin motor domain homology <KWOT> F;147-154/Region: nucleotide-binding motif A (P-loop) F;153/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKVPYDAIISEELLMKDPNYKLKDED-----IVNEVKGGYVIKVDGKYYVYLKDAAHADN
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                                                          VKTCTTSLNDADII-LSDYISDQKSKFESKQQDLIANIGKIVSNFLQEQNESLYTK----
                                                                                                                                                                      MSSQKLGNGISSELIELQKDMKESYRQLVQELRSLYNLQHTHEESQKELMYGVRNDIDAL
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                                                                                                                                                                                                                                                                                    QLLISMTKITEHFQSLDEALQSARSSCAVPNSSLDLIVSELKDSKNSLLDALEHSLQDIS
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LPPSPDADVKANPTGDSAAAI--YNRVKGEKRIPLVR------LPYMVEHTVEVK
                                                                                                              ADKYTTS---DGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGI
                                                                                                                                                                                                                             -HPERLGKPNS------
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Search completed: November 14, 2003, 10:37:44 Job time : $67\ \text{secs}$

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SLEM_BACBR
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PGCV_MOUSE
IGA_NEIGO
YMX6_YEAST
TCP8_HUMAN
RIN4_RAT
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SPCA DROME
SPCA DROME
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YMJB CAEEL
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GTFC STRMU
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SNF2_YEAST MSP1_PLAFW USO1_YEAST

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murakami Y., Naitou M., Hagiwara H., Shiba
Sasanuma S.-I., Sasanuma M., Tsuchiya Y.,
Yamazaki M., Tashiro H., Eki T.,
"Analysis of the nucleotide sequence of ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=S288c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Hypothetical 137.7 kDa protein in UGS1-FAB1 i.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S288C / AB972;
MEDLINE=95400292; PubMed=7670463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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  KDNLVLEDEAEAPTQENKPTEVVGEIDIPDAPRDD-----VEIVEAVEKNIIPEDLEVAK
                     --HWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISR
                                            QEAVRNNEVSGTEEESTSKGEEIMGGD
                                                                                       RETYDDETMGPTKRISDNEKNLQHGTNDISVEVEKEEEEEEEEENSTFSKVKKENVTGE
                                                                                                                                  PSVLAKNQKETEIGKEDHVFEQKDKEDEKCRKELSVNHENNMSHNFNAAGSDSIIPPETE
                                                                                                                                                        NSRTYRRQNSDNTSRTNWVPSVSNP-----GTTNTNTSNNSNTNSQASQSNDI-----
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participates in amiloride-sensitive sodium channel activ

J. Cell Biol. 119:1497-1506(1992).

-:- FUNCTION: IS PART OF A MULTIMERIC COMPLEX WHICH IS I

AMILORIDE-SENSITIVE SODIUM CHANNEL ACTIVITY.

-:- SUBCELLULAR LOCATION: Membrane-associated.

-:- TISSUE SPECIFICITY: KIDNEY, PROXIMAL INTESTINE, OOCY
TO LESSER EXTERNOLUTES DISTAL INTESTINE, STOMACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staub O., Verrey F., Kleyman T.R., Kraehenbuhl J.-P.;
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Q01613;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seq
15-JUL-1998 (Rel. 36, Last ann
                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                    or send an email to license@isb-sib.ch).
                                                                                   entities requires a license agreement
                                                                                                            modified and this statement
                                                                                                                                                                                                                                                                                               -!- SIMILARITY: SOME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Primary structure of an apical protein from Xenopus
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                            RSAGASSSYDATVTWNDRFGKTSPLGRSAAEKTAGVQRK---TFSDQRTLDGSQEH----
                                                                                  QHNALVQYMERKTNQRPNSN----PQVQMERTSLGLPNYNEWSIYSSETSSSDASQKYLRR
                                                                                                             DH-----SEDPNKNFKADEEPVEETPA----
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Matches 173
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PROSITE; PS00972; UCH 2 1; 1.
PROSITE; PS00973; UCH 2 2; 1.
PROSITE; PS00973; UCH 2 3; 1.
UCH 2 3; 1.
UCH 2 3; 1.
UCH 2 3; 1.
COMAIN 195 313
ACT_SITE 786 786
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P40818;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41; Last annotation update)
Ubiquitin carboxyl-terminal hydrolase 8 (EC 3.1.2.15) (Ubiquitin thiolesterase 8) (Ubiquitin-specific processing protease 8)
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ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Res. 1:223-229(1994).
-!- CATALYTIC ACTIVITY: Ubiquitin C-terminal ubiquitin + a thiol.
-!- SIMILARITY: Belongs to peptidase family (-!- SIMILARITY: Contains 1 rhodanese domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Seki N., Kawarabayasi Y., Ishikawa K.-I., Tabata S., "Prediction of the coding sequences of unidentified human The coding sequences of 40 new genes (KIAA0041-KIAA080) analysis of cDNA clones from human cell line KG-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00581; Rhodanese; 1. Pfam; PF00443; UCH; 1.
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GO:0004197; F:cysteine-type endopeptidase
GO; GO:0004843; F:ubiquitin-specific protease
GO; GO:0008283; P:cell proliferation; TAS.
GO: GO:0007048; P:oncogenesis; TAS.
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Genew; HGNC:12631; USP8.
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MEDLINE=96051398; PubMed=7584044;
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InterPro; IPR001394; UCH-2.
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                                                                                                                                                                                                 RHODANESE.
BY SIMILARITY.
BY SIMILARITY.
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DE DnaJ-1
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OS MYCDI
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Mycoplasma pneumoniae.

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PROSITE; PS00636; DNAJ 1; 1.
PROSITE; PS50076; DNAJ 2; 1.
Hypothetical protein; Chaperone; Complete proteome.
DOMAIN 4 73 J-DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000004; AAB95683.1; -. PIR; S73361; S73361.
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Himmelreich R., Hilbert H., Plagens H.,
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MEDLINE=97105885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00226; DnaJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete sequence analysis of the genome
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SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P25685; 1HDJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; PR00625; DNAJPROTEIN SM00271; DnaJ; 1.
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FSSFVLSDQNPNPQTPTHHEEDAAAPEPTVDETSGESTAPEVTIAESTVELETAAEINNP
                                               LLAFL-----APITHPERLGKPNSQI-----EYTEDEVRIAQLA----
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                                                                                                                                                                                                                                                                    DSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKK 429
                                                                                                                                                                                                                                                                                                                                                                                                                                   GQWVWLEETEPSSVSNDETTTDSDAVTAATT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRONSDNTSR
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                                                                                                                                                                                                               TTSAVEMDASVK----ADVSDEADATNEPTEQDTISEPEQ--ETDAAALEEINHT-TADL
                                                                                                                                                                                                                                                                                                                                                                              IPLRYRSNHWVPDSRPE-----QPSPQPTP-----EPSPGP-----QPAPNLKI 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -KQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARI
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Hsp_DnaJ.
                                                                                                    SATNDLEQDVVEKVNFSEPESTVDTAATDPVVEQATETSTNGFKFF-N
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Pred. No. 0.43;
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                                                                                                 Query Match
Best Local :
                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YM67 YEAST STANDARD; PRT; 1658 AA. 003661; Q04988; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Hypothetical 187.1 kDa protein in GUA1-ERG8 in YMR219W OR YM8261.13 OR YM9959.01.
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YM67_1
                                                                                                                                                                                                     EMBL; Z49809; CAA89934.1; -.
EMBL; Z49939; CAA90190.1; -.
PIR; S55101; S55101.
SGD; S0004832; ESC1.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0006348; P:chromatin silencing at telomere;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome"
                                                                                                                                                                 Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatice Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 387:90-93 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9169872;
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                                                                                                 Similarity
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1658 AA;
                                                                            Conservative
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Pred.
                                                                       Mismatches
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No. 0
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RESULT 6
SC16 YEAST STANDARD; PRT; 2195
ID SC16 YEAST STANDARD; PRT; 2195
AC P48415; Q02822;
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence updated)
DT 28-FEB-2003 (Rel. 41, Last annotation upon the continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous contin
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    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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                                                                                                                                               Query Match
Best Local (
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                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                      SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                   SEQUENCE
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EMBL; U41849; AAB68254.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The nucleotide sequence of Saccharomyces cerevisiae Nature 387:103-105(1997).
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SUBCELLULAR LOCATION: ON THE ENDOPLASMIC RETICULUM AND ON VES
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STNISPANETQLEIPDTQELHHKLLNDSDQHDITADSNDLPDNSIVEHDSVITQT-KPAM
                                                                 HSEEPLELPESTINSS.
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                               NNSNTNSQASQSNDI - - - - - -
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                                                                                               KKASRYKPIIEE---EAGMRQEQVHFTNTT
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G. Warl J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1991 (Rel. 20, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
205 kDa microtubule-associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DROME
                                                                                                                                                                                   MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                      STRAIN=Berkeley;
                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                         Irminger-Finger I., Laymon R.A., (
"Analysis of the primary sequence the Drosophila 205K MAP.";
                                                                                                                                                                                                                                                                                                               MEDLINE=91115949; PubMed=1703540; Irminger-Finger I., Laymon R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly)
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Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Fosler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Go Z., Gubart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Go Z., Gubart W.M., Glasser K., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLeodd M.P., McPherson D., RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Na Melson K., Nusoka M.P., McPherson D.L., RA Meison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Shue B.C., Siden-Riamos J.A., Weinstock G.M., Weissenbach J., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Yang S., Yao Q.A., Sheng Y.-Yang S., Yao Q. A., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Zhan M., Zhang G., Zhao Q., Zheng L., RA Wang Z.-Y., Zhong W., Zhong W., Zhou X., Smith H.O., RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., Tha Q., Zheng L., First M., Wang Y., Wang A., Wang Z.-Y., Zhong W., Zhou X., Smith H.O., Ra Gibbs R.A., Wang Z.-Y., Wang Y., Wang Y., Wang Y., Wang Y., Wang 
Query Match
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Matches 163;
                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as modified and this statement is not removed. It entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
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Durbin K.J., Evangelista C.C., Ferraz C.,
                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
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Base; FBgn0002645; Map205.
GO:0005875; C:microtubule associated complex; ID;
GO:totobules; Alternative splicing; Phosphorylation.
ASP/GLU-RICH (ACIDIC).
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MISCELLANEOUS: PHOSPHORYLATION OF VARIOUS SERINE RESIDUES MAY PLA?
A REGULATORY ROLE. THE BASIC DOMAIN CONTAINS NUMBEOUS SEQUENCES
THAT MATCH KNOWN CONSENSUS SEQUENCES OF SEVERAL DIFFERENT PROTEIN
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745
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        Conservative
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Score 156.5; D
Pred. No. 0.66;
1; Mismatches
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Missing (in isoform
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ASP/GLU-RICH
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FTId=VSP_004321.
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        304;
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                                                                                 Length 1185;
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                               NNSIMAEAEKLLALLKGSNP-SSVSKEKI
                                                                                                 KVEA-----QLKEAEVLLAKVTDSS----LKANATETLAGLRNNLTLQIMD------
                                                                                                                                  RVASEQNDE---ENAVFESVSGYETQNFDEISSPPEGINPFAQPF--TPAHLVIEQANTM
                                                                                                                                                                                                    TAEKHLVEDTKELVEEYTLDP-ESHFFGVV-----SSQAPLQLFGKHTLPSIIHSCKH
                                                                                                                                                                                                                                    ---PYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAP----NGYTLEDLFATIKY
                                                                                                                                                                                                                                                                     QMQL-PAECSDIFADQSLLLDTSAP---QLSSEADSPVAKLELESQQAGIVDITPSPLSS
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                                                                  MEDVGGMPIPASEDFAICDKVASKSSNEVEDHRSEQQAFVKEELLHPVGDVVAQVENLGT
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RESULT
ANK2_HU
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Q01484; Q01485;
01-APR-1993 (Rel. 25, Created)
01-OCT-1996 (Rel. 34, Last seque
28-FEB-2003 (Rel. 41, Last annotation)
Ankyrin 2 (Brain ankyrin) (Anky
                                                                                                                                      HUMAN
                              Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                             ANK2.
SEQUENCE FROM N.A.
(ISOFORMS
                              Chordata;
Primates;
                                                                                  Last sequence update)
                                                                         (Ankyrin
1; 2 AND
                              Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                         œ 5
                                                                                                                            3924
                                                                     update)
(Ankyrin,
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                               Hominidae;
                                                                       nonerythroid).
                                          Euteleostomi;
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PRINTS; PRO1415; ANKYRIN.
SMART; SM00248; ANK; 22.
SMART; SM00005; DEATH; 1.
SMART; SM000218; ZU5; 1.
SMART; SM00218; ZU5; 1.
PROSITE; PS50008; ANK REPEA
PROSITE; PS50007; ANK-REP R
PROSITE; PS50017; DEATH_DOW
                                                                                                                                                                                                                                                                                                EMBL; X56957; CAA40278.1; -...
EMBL; X56958; CAA40279.2; -...
EMBL; Z56634; CAB42644.1; -...
EMBL; M37123; AAA63828.1; -...
PIR; S37431; S37431.
                                                                                                                            InterPro; IPR000488; Death. InterPro; IPR000906; ZUS. Pfam; PF0023; ank; 23. Pfam; PF00531; death; 1. Pfam; PF00791; ZUS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 463-495 FROM N.A.

MEDLINE=92009921; PubMed=1833308;

TSE W.T., Menninger J.C., Yang-Reng T.L.

Lux S.E., Ward D.C., Forget B.G.;

"Isolation and chromosomal localization ankyrin gene.";
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                                                                                                                                                                                                                                                                                     HSSP; P42771;
                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM
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Submitted
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MEDLINE=91302466;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q01484-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q01484-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ., Kordeli E., Bennett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    soId=Q01484-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kunimoto M., McLaughlin T., Bennett V.; ion and characterization of cDNAs encoding s reveal a family of alternatively spliced Biol. 114:241-253(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION (POTENTIAL)
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                                                        67 HYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHADNV
                                                                                7 YQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHY
                                                                                                  Similarity
DSVSEEV--
                                                                    FEARVKEEEQK---IFGLMVDRQSQGTTPDTTPARTP
           DTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDN-----
                                  RTKEEINRQKQEHS---QHREGGT-----
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Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                        JOVOV B., Ripoil P.J., Benos D.J.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical KIAA0373.
                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Trachea;
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[ protein KIAA0373.
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Similarity 18.5%;
71; Conservative 124
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                            EKAEVERKLGRVRGSGRSGKTIPELEKTIGLMKKVVEKVQRENEQLKKASGILTSEKMAN
                                                                              EKVEAQLKEAEV---
                                                                                                                             TSGIDSDDHYQREQELQRENLKLSSENIELKFQLEQANKDLPRLKNQVRDLKEMCEFLKK
                                                                                                                                                                            EHVLGKKDH----SEDPNKNFKADEEPVE----ETPAEPEVPQVET---
                                                                                                                                                                                                                                LDLENDISYMRSHQA-----
                                                                                                                                                                                                                                                                               LIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVE--HPDERPHSNDGWGNAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                  KSAREEVIRWEEGKKWQTKIEGIRNKLKEKEGEVYI---LTKQLTTLKDLFAKADKEKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYTTSDGY1FDE------HDIISDEGDAYVTPHMGHSHWIGKD--SLSDKEKVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RQIKRLTSGLQGKPLIDNKQSLIEEL-----QKKIKKLESQLERKVDEAEMKPMKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLLERLNDE-----STNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLAD
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Pred. No. 1.2;
24; Mismatches
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COILED COIL (POTENTIAL).
MW; 03CBA02A64CF4139 CRC64;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O., "Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain we code for large proteins in vitro.";
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DOMAIN
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Mammalia; Eutheria;
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IVKKHEEDLHILHHRLELQADSSLN-----KFKQTAW--DLMKQSPTPVPTNKHFIRLAE
                                  VAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPT---
                                                                      KSHHTLKIAHQTIANMQA-RLNQKEEVLKKYQRLLEKAREEQ
                                                                                                          GTTNT-NTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARG
                                                                                                                                              ATCKSLEEKLKEKESALRLAEQNILSRDKVINE--LRLRLPATAEREKLIAELGRKEMEP
                                                                                                                                                                                                                      LDIFDRQQNEILNAAQKFEEATGS---IP-
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Tzermia M., Kattoulou C., Alexandraki D.;
"Sequence analysis of a 33.2 kb segment from the left arm of chromosome XV reveals eight known genes and ten new open read frames including homologues of ABC transporters, inositol phosphatases and human expressed sequence tags.";
Yeast 13:583-589(1997).
                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                               MEDLINE=97321807; PubMed=9178509;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                      -!- SIMILARITY: BELONGS TO THE SINI FAMILY.
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                                                                                                                                                                                                                                                                                                                                        SHWIGK-----DSLSDKEKVAAQAYTKEKG---ILPPSP-----DAD-VKANPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLTAKKENVAP------RDQEFYDKAYNLLTEAHKA----LFXNKGRNSDFQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPLNSYLKADAGGAVAA----
                               KVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKL-----LALLKGSNPSSVSKEK
                                                                      LGKNYILDLNDTVLRLDGINKVELISKKDARELHLEKMKPDLKKPVLPTIQSNDLTPLTL
                                                                                                                                                   NVNPKFNYTTISVLVT
                                                                                                                                                                                      N-----GYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGK--KDHSEDPN-----
                                                                                                                                                                                                                                                             DSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAP
                                                                                                                                                                                                                                                                                                     ---FGKLDRKSTIQSISDSEVVLCKVDDAEKSQNEIETPLPFETGGGLMDASTLDANSSH
                                                                                                                                                                                                                                                                                                                                                                                                                   ERLGKPNSQIEYTEDEVRIAQLAD-----KYTTSDGYIFDEHDIISDEGDAYVTPHMGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKIFLTDNK-----NDGQKSDSLNANKGI-----HGDGSSASGNGSVSRDGLTETE
                                                                                                                                                                                                                            DTTDGTINQLSFYK--PIIG----NEDDIDKTNGSKII
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Pred. No. 1.4;
18; Mismatches
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 - I PENTKVTSKAKKI STKYKLGLAKQHSSSVASGS
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MEDLINE-95104449; PubMed=7805871;

L'Abbe D., Banville D., Tong Y., Stocco R.,

Fantus G., Shen S.H.;

"Identification of a novel protein tyrosine homology to the cytoskeletal proteins of the FEBS Lett. 356:351-356(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTINL RAT STANDARD; PRT; 1175 AA. 062728; Q62732; O1-NOV-1997 (Rel. 35, Last sequence update) Protein tyrosine phosphatase, non-receptor tylenter phosphatase 2E).

PTINL RAT STANDARD; PRTP AA. 062728; PROTEIN CARPORE PROSPHATASE 2E).
                                                                   PROSITE; PS00660; FERM 1; 1.

PROSITE; PS00661; FERM 2; 1.

PROSITE; PS00661; FERM 3; 1.

PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.

PROSITE; PS00383; TYR_PHOSPHATASE_PTP; 1.

PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.

Structural protein; Cytoskeleton; Hydrolase; Alternative splicing.
                                                                                                                                                                                                                                                   Pfam; PF00102; Y_phosphatase;
PRINTS; PR00935; BAND41.
PRINTS; PR00700; PRTYPHPHTASE
SMART; SM00295; B41; 1.
SMART; SM00194; PTPC; 1.
                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000299; Band 4.1.
InterPro; IPR000387; TYR Dhosphatase.
InterPro; IPR000242; Tyr PP.
Pfam; PF00373; Band 41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOId=063728-2; Sequence=VSP 000498;
-i- TISSUE SPECIFICITY: PARTICULARLY ABUNDANTLY IN
-i- SIMILARITY: CONTAINS 1 FERM domain.
-i- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S51005; S51005.

    -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate
tyrosine + phosphate.

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Sciurognathi;
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Q1-APR-1993
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SEQUENCE FROM N.A.
MEDLINE=92315338; PubMed=1617731;
Galinski M.R., Medina C.C., Ingra
                                                                    Plasmodium vivax (str
Eukaryota; Alveolata;
NCBI_TaxID=31273;
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                                                                                                                 Belem)
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-!- FUNCTION: INVOLVED IN RETICULOCYTE ADHE HUMAN RETICULOCYTE CELLS.
-!- SUBUNIT: Homodimer (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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    -!- SUBCELLULAR LOCATION: Membrane-bound.

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|GYI-
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                                                          SKKLIMINKEKENTEKCVD
                                                                                                                                   MRNISEKIS-
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                                                                                                                                                                                                                                                                                    EVVSEKVREALKRLSQVEGIRCHFENFHRLLDNTBELENLKKMVTI-YR-----DKKSE
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                                                                                      DKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTS
                                                                                                                                                                                                              RES--
                                                                                                                                                                                                                                                                                                                     FDPAQITSRTARGVAVPHGDHYHFIPYSQM----SELEERIARIIPLRYRSNHWVPDSRPE 347
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-PDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKE 575
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CYTOPLASNIC.

CELL ATTACHMENT SITE (POTENTIAL)

CELL ATTACHMENT SITE (POTENTIAL)
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Mismatches
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               RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamiin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamiin N., Harris D., Hidalgo J., Hodgson G.,
RA Gontles S., Goble A., Hamiin N., Harris D., Hidalgo J., Hodgson G.,
RA Gollver K., Owell S., Murgall K., Murphy L., Niblett D., Odell C.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woltyens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadleu B., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.C., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
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P24339;
01-MAR-1992
01-OCT-1996
28-FEB-2003
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CUT7_S
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Nature 347:563-566(1990)
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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CUT7 OR SPAC25G10.07C.
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Cruzado L.,
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(Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
Motor protein; Cell division; Microtubules; ATP-binding; Coiled
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GeneDB_SPombe; SPAC25G10.07c; -.

InterPro; IPR001752; kinesin_motor.
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EMBL; Z70691; CAA94636.1; -.
EDIR; T38378; T38378.
                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
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SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. BIMC
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                                       NALVEKAHHIPYRESKLTRLLQDSLGGKTKTSMIVTVS---STNTNLEETISTLEYAARA
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Pred. No. 2.
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SASNPRKRAEEPTIDTGYPDRSDTNSPT LRAILGNDVSLLLLTL (IN REF. 1).
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
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YNJ1_YEAST
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                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
               This
                                             MEDLINE=96367601; PubMed=8771715;

Garcia-Cantalejo J.M., Boskovic J., Jimenez A.;

Gaycia-Cantalejo J.M., Boskovic J., Jimenez A.;

"Sequence analysis of a 14.2 kb fragment of Saccharomyces cerevisiae chromosome XIV that includes the ypt53, tRNALeu and gsr m2 genes and four new open reading frames.";

Yeast 12:599-608(1996).

-!- SIMILARITY: TO S.POMBE SPAC29E6.10C.
                                                                                                                                                                 STRAIN=S288c
                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                               YNL091W OR N2231.
                                                                                                                                                                                                             _TaxID=4932;
SWISS-PROT entry is copyright. It is produced ten the Swiss Institute of Bioinformatics and
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S52734; S52734.
SGD; S0005035; YNL091W.
GO; GO:0009651; P:salinity response;
Hypothetical protein.
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Pred. No. 2.7;
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ID JIP3_MOUSE
N [5]

RY SEQUENCE OF 1240-1337 FROM N.A.

RY SEQUENCE OF 1240-1337 FROM N.A.

RY MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                Q9ESN9; Q99KU7;
Q9R0U7;
28-FEB-2003 (Rel
                                                                                                                                                                                                                                                                 (SYD)
Cell
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIFICITY, SUBCELLULAR LOCATION, PHOSPHORYLATION, MARG-205; PRO-206; THR-207; SER-208; LEU-209; THR-266; THR-287, AND INTERACTION WITH MAPK8IP2; MAPK8; MAPK9; AND MAP3K11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99455010; PubMed=10523642; Ito M., Yoshioka K., Akechi M., Yamashita Sugiyama K., Hibi M., Nakabeppu Y., Shiba "JSAP1, a novel jun N-terminal protein kin that functions as a scaffold factor in the Mol. Cell. Biol. 19:7539-7548(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
C-jun-amino-terminal kinase interacting protein 3 (JNK-interacting protein 3) (JNK-interacting protein 3) (JNK-interacting protein 3) (JNK-interacting protein 3) (JNK-interacting protein 3) (JNK-interacting protein 3) (JNK-interacting protein 3) (JNK-interacting protein 3) (JNK-interacting protein 3) (JNK-interacting protein 3) (JNK-interacting protein 3) (JNK-interacting protein 3)
                                                                                                                                                                                                                                                                                                                                   MEDLINE=20560743; PubMed=11106729; Bowman A.B., Kamal A., Ritchings B Gindhart J.G., Goldstein L.S.B.;
                                                                                                                                                                                                                                                                                                                   Gindhart J.G., Goldstein L.S.B.;
"Kinesin-dependent axonal transport
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20094982; PubMed=10629060; Kelkar N., Gupta S., Dickens M., D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              splicing.";
Gene 255:229-234(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6; TISSUE=Brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ito M., Akechi M., Hirose R., Ichimura M., Takamatsu N., Xu P.,
Nakabeppu Y., Tadayoshi S., Yamamoto K.-I., Yoshioka K.;
"Isoforms of JSAP1 scaffold protein generated through alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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abeppu Y., Tadayoshi S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           eraction of a mitogen-activated the neuronal protein JIP3."; Cell. Biol. 20:1030-1043(2000).
                                                                                                                                                                                                                                                                                 ) protein.";
103:583-594(2000)
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; Q9EQD8; Q9ESN7;
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Rodentia;
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Sciurognathi; Muridae;
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Yamamoto K.-I.;
(JNK)-binding pr
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                                                                                                                                                                                                                                                                                                                    the
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; Murinae; Mus
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pathway.";
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Whiting M. Blakesley
                                                    EMBL;
                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                          or send an
                                                                                                     entities requires a
                                                                                                                      modified
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"Cargo of kinesin identified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21135887; PubMed=11238452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERACTION
                                                                                                                                                                                                                   and kidney. All isotorms have been and lung. Mapk8ip3A is also expressed in the spleen and lung. INDUCTION. Expressed in neurities 5 days following initiation of nerve growth factor Ngf induced differentiation. Ngf withdrawal nerve growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pathway namely Mapk8, Mapk9 and Mapk10 to the N-terminal region Map2k4 and Map2k7 to the central region and Map3k11 to the C-terminal region. Binds the TPR motif-containing C-terminal of kinesin light chain, pre-assembled Mapk8ip1 scaffolding comple are then transported as a cargo of kinesin, to the required subcellular location. Subcellular location. Subcellular location cytoplasmic; localised in the soma and growth cones of differentiated neurites and the Golgi and vesion fithe early secretory compartment of epithelial cells. Alternative splicing; Named isoforms=6;
                                                                                                                                                                                                  mediated cleavage.
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: Highly expressed throughout many regions the brain and at lower levels in the heart, liver, lung, test and kidney. All isoforms have been identified in the brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          region of Mapk8ip3 interacts with the C-terminal of Mapk8ip2 not Mapk8ip1. Binds specific components of the JNK signaling
                                                                                                                                                                                                                                                                                                                                    Name=1e
                                                                                                                                                                                                                                                                                                                                                                                                                 Name=1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=1c; Synonyms=3b;
AB005662; BAA85874.1;
AB043124; BAB16675.1;
AB043125; BAB16676.1;
AB043123; BAB16674.1;
AB043129; BAB16685.1;
AB043129; BAB16685.1;
                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9ESN9-4;
                                                                                                                                                                                                                                                                                                                     IsoId=Q9ESN9-6; Sequence=VSP_002776;
                                                                                                                                                                                                                                                                                                                                               IsoId=Q9ESN9-5;
                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9ESN9-3;
                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q9ESN9-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9ESN9-1;
                                                                                                                   non-profit institutions as long and this statement is not removed.
                                                                                        equires a license agreement (Semail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WITH KLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Madan A.,
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence=VSP_002776,
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                                                                                                                                                                                                                                                                                                                                             Sequence=VSP_002778,
                                                                                                                                                                                                                                                                                                                                                                        Sequence=VSP_002775;
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence=VSP_002775,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence=Displayed
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                                                                                                                                                                                                   SCAFFOLD
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                                                                                                       (See http://www.isb-sib.
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GO; GO:00198
GO; GO:00050
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GO; GO:00163
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Alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO:0016192;
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AB043128; BAB16685.1;
AF178637; AAF26843.1;
AF178636; AAF26842.1;
AF262046; AAG36931.1;
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                                  214
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tive splicing, Phosphoxylation, Coiled coil.

COLLED COIL (POTENTIAL).

266 266 PHOSPHORYLATION (BY MAPK).

287 287 PHOSPHORYLATION (BY MAPK).

288 287 287 PHOSPHORYLATION (BY MAPK).

298 287 287 PHOSPHORYLATION (BY MAPK).
                                                                                                                                                                                                                                                         Similarity
 TSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKL--
                                    LADGMVRAQMGGKLVPAGDHWH---
                                                                    NASDII EDTGDAYI VPHGDHYHYI PKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDN
                                                                                                   SEMKKEYNALHQRHTEMIQTYVEHIERSKMQQVGGSGQTESSLP-GRSRKERPTSLNVFP
                                                                                                                                      NRQKQE----HSQHRE-----
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COILED COIL (POTENTIAL).
PHOSPHORYLATION (BY MAPK).
PHOSPHORYLATION (BY MAPK).
PHOSPHORYLATION (BY MAPK).
Missing (in isoform la and i
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PHOSPHORYLATION (BY M
Missing (in isoform 1
/FTId=VSP_002775.
                                                                                                                                                                                                                                                                                                    OF MAPK8193; WHEN ASSOCIATED WITH AND A-287. DOES NOT EFFECT BINDING PROPONENTS OF THE JIK PATHWAY.

K -> R (IN REF. 4).

F -> L (IN REF. 3; AAF26843).

E -> K (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                        AND A-287. DOES NOT EFFECT BINDING OF COMPONENTS OF THE JNK PATHWAY.
T->A: RESULTS IN LOSS OF PHOSPHORYLATION
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A: RESULTS IN LOSS OF PHOSPHORYLATION
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01-FEB-1996
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P47534;
SEQUENCE FROM N.A.

STRAIN-ATCC 33530 / G-37;

MEDLINE=96026346; PubMed=7569993;

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Frischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.I.

Fritchman J.L., Weidman J.F., Small K.W., Phillips C.A., Merrick V.

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Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).

-i- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP +
                                                                                                                                                                                                                                       Mycoplasma genitalium 
Bacteria; Firmicutes;
                                                                                                                                                                                                                    NCBI_TaxID=2097;
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13 (Rel. 41, Last a
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annotation update)
6.1.1.7) (Alanine--tRNA
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694 667 612 600 574 559 518 521 458

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Matches 127
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InterPro; IPR002318; tRNA-synt_2c.
InterPro; IPR00193; tRNA_synt_Ala.
Pfam; PF01411; tRNA-synt_2c; 1.
PRINTS; PR00980; TRNASYNTHALA.
PRINTS; PR00980; TRNASYNTHALA.
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PROSITE; PS50860; AA_TRNA_LIGASE_II_ALA; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U39709; AAC715
PIR; C64232; C64232.
TIGR; MG292; -.
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SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
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127; Conserv
                                           TETLAGLRNNLTLQIMDNNSIMAEA----EKLLALLKGSNPSSV
                                                                                                                                                                                                                              FDDHTYK-----APNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSED
                                                                                                                                                                                                                                                                            LNRHLTRNELEKVENKIRSLIKQKISSKEIFTDFEGSQKLNAIAYFEEEYSQHEILRVIR
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SDTLLALKNDINQLKTKNYKVSQQALALSIKKQLLSLVDENKSYV
                                                                                         INNYLKAENQKLIQLKSELEKVLSLIDSSIFKVELKELQQRLDKFILPEKITQ---LRDA
                                                                                                                                       PNKNFKADEEPVEETPAEPE---VPQVETEKVEAQLKEAE------VLLAKVTDSSLKANA
                                                                                                                                                                                     FGDYSVELCGGTHVANTASIEDCFITDFYSL-----
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-!- FUNCTION: REQUIRED FOR MEJOTIC CHROMOSOME SYNAPSIS AND CELL CYCL PROGRESSION. MAY ACT AS A MOLECULAR ZIPPER TO BRING HOMOLOGOUS CHROMOSOMES IN CLOSE APPOSITION. ZIPI MAY ENCODE THE TRANSVERSE FILAMENTS OF THE SYNAPTONEMAL COMPLEX.
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01-OCT-1996 (Rel. 34, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
Synaptonemal complex protein ZIP1.
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DOMAIN 177 333
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STRAIN=BR1824-3B;
MEDLINE=93161412; PubMed=7916652;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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$0002693; ZIP1.
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16-OCT-2001 (Rel. 40, I
28-FEB-2003 (Rel. 41, I
                                                                                                                                                                                       SCHPO
                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                          Protein sts5.
STS5 OR SPCC16C4.09.
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                                                              Schizosaccharomycetes;
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Comnor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Comnor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Mooney P., Moule S., Mingall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mingall K., Murphy L., Niblett D., Odell C.,
RA Galler C., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Waltjens I., Vonstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moore V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aces S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., McCombie W.R., Paulsen I., Potashkin J.,
RA Gariutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RL Mature 415.871-880 (2002).

CC Grympal C. Schizosaccharomyces pombe.";

RE GC Grympal C. Schizosaccharomyces pombe.";
                                                                      Matches
                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                      Hydrolase; Nuclease; Exonuclease.
CONFLICT 5 5 F ->
CONFLICT 794 794 V ->
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J. Cell Sci. 109:2331-2342(1996).
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                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                  GeneDB SPombe; SPCC16C4.09; -.
InterPro; IPR001900; Ribonuclease_II.
Pfam; PF00773; RNB; 1.
                                                                                                                                                                                                                                                                                                                                                 PIR; T41099; T41099.
PIR; T45283; T45283.
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SUBUNIT: INTERACTS WITH SERINE/THREONINE PHOSPHATASE PPE1, KINASE C AND AN OSMOSENSING MAP KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the ribonuclease II (RNB) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Cytoplasmic.
186 VPHGDHYHYIPKNELSASELAAAE-AFLSGR----
                                                                                              Similarity
                                                                                                                                                                                                                                                       PS01175; RIBONUCLEASE_II; FALSE_NEG
                                                                                                                                                                  1066 AA;
                                                                        Conservative
                                                                                                                                                             5 F -> C (IN REF. 1).
94 V -> G (IN REF. 1).
117602 MW; 077187800B330C15
                                                                                              21.9%;
                                                                                                                  3.4%;
                                                                      69;
                                                                                              Score 142.5;
Pred. No. 3.2
                                                                        Mismatches
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                                                                                                                  DB 1;
                                                                        192;
                                                               indels 131;
                          GNLSNSRTYRRQNSDNTSR 234
                                                                                                                  Length
                                                                                                                                                                  CRC64;
                                                                                                                       1066;
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D7_B1688;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=5080502; PubMed=7988791;
Agarwal A., Sloger M.S., Oyama M., Blumberg D.D.;
"Analysis of a novel cyclic Amp inducible prespore
Dictyostelium discoideum: evidence for different pa
regulation.";
Differentiation 57:151-162(1994).
-!- DEVELOPMENTAL STAGE: EXPRESSED SPECIFICALLY IN
                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the Buropean Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=AX3
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                                                                     Sporulation;
                                                                                         DictyDb;
                                                                                                                  EMBL; U25143; AAA73514.1;
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TANA_XENLA
Baraga
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TANA XENLA Q01550; Q1-JUN-1994 01-JUN-1994 16-OCT-2001

(Rel. (Rel.

29, Created)
29, Last sequence 40, Last annotations

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       LOEVED
                             LAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSVSKEKI
                                                                                 SNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKEAEVL
                                                                                                                                                                                                                                                                           ---DKEQLIDLQNREPGLYKNQ----QDLK------QEKRANQQELI---
                                                                                                                                                                                                                                                                                                     FYDKAYNL-LTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITH
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                                                         LNDANDNFEQVNNNNNNINNNNNNNNFKVDKS
                                                                                                             DNTHNT
                                                                                                                                      VEHTVEVKNGNLI I PHKDHYHNI KFAWFDDHTYKAPNGYTLEDLFATI KYYVEHPDERPH
                                                                                                                                                                                          KDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYM 617
                                                                                                                                                                                                                                                PERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIG
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16.7%;
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-APERLYEEIHNSNL-----NKAVQEAEEIERQQNGNGSPAVNSHKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GQVAITAKDSLGATITGLGGVSSTAKVGGQITNGRAQGQVITGG
                                                                                                             PFODDYHNDOTEELKD
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Pred. No. 2
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Query Match
Best Local S
Matches 144
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuron 9:417-428(1992).
-!- TISSUE SPECIFICITY: GROWTH CONES OF EMBRYONIC VERTEBRATE NEURONS
-!- DEVELOPMENTAL STAGE: IS EXPRESSED IN THE NEURULA AND PERSIST DURING EMBRYOGENESIS IN THE BRAIN, CRANIAL NERVES, AND SPINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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MEDLINE=92398961; PubMed=1524825;
Hemmati-Brivanlou A., Mann R.W., Harland R.M.;
Hemti-Brivanlou A., Mann R.W., Harland R.M.;
"A protein expressed in the growth cones of embryonic vertebrate
"A protein expressed in the growth cones of embryonic vertebrate
"neurons defines a new class of intermediate filament protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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-- INEQECLKSDQIREAFDTEEV-
                                  KLPLSQRHVESDGL--VFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPL
                                                                                                   GNLSNSRTYRRONSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSOASQSNDIDSLLKQLY
                                                                                                                                                                         LARSOGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGR 215
                                                                                                                                                                                                                                              EVKGGYVIKVDGKYYVYLKDAAHADNVRTKEEI----NRQKQEHSQHREGGTPRNDGAVA
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1PR001664; IF.
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COIL 1B.
LINKER 12.
COIL 2A.
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COIL 1A.
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Pred. No.
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6.7;
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                                                                                                                                Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth Bowman K., Devlin K., Gentles S., Hamlin N., Hunt S. Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosom
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01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEAST
                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                          STRAIN=S288c;
Madison J., Winston F
Submitted (APR-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                              STRAIN=S288c
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               Zinc finger protein MOT3/HMS1.
MOT3 OR HMS1 OR YMR070W OR YM9916.09
                                                                                                        Nature 387:90-93(1997)
                                                                                                                                                                                                            PubMed=9169872;
                                                                                                                                                                                                                                             SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                     SUBCELLULAR LOCATION: Nuclear (Potential).
SIMILARITY: Contains 2 C2H2-type zinc fingers.
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RESULT 23
MYS1 YEAST STANDARD; PR
ID MYS1 YEAST STANDARD; PR
AC P08964;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1995 (Rel. 31, Last seque
DT 16-OCT-2001 (Rel. 40, Last annot
DE Myosin-1 isoform (Type II myosin
GN MYO1 OR YHR023W.
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SGD; S0004674; MOT3
GO; GO:0005634; C;
GO; GO:0003677; F:C
GO; GO:0016564; F:C
GO; GO:0006350; P:C
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Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
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SMART; SM00355; ZhF C2H2; 2.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.

Nuclear protein; Zinc-finger; Metal-binding;
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GO:0005634; C:nucleus; IDA.
GO:0003677; F:DNA binding activity; IPI.
GO:0016564; F:transcriptional repressor activity; IDA.
GO:0016560; P:transcription; IGI.
GO:0006350; P:transcription; IGI.
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Similarity 19.3%;
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InterPro; IPR001609; myosin head.
Pfam; PF00063; myosin head; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin head; 1.
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GO; GO:0000142; C:contractile ring (se GO; GO:0007120; P:caxial budding; IMP.
GO; GO:0016288; P:cytokinesis; IMP.
GO; GO:0016289; P:response to osmotic
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EMBL; X06187; CAA29550.1; -.
EMBL; U10399; AAB68872.1; -.
PIR; S46773; S46773.
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MEDLINE=9108308; PubMed=2263482;
Sweeney F.P., Watts F.Z., Pocklington M.J.,
"The MYO1 gene from Saccharomyces cerevisiae
sequence.";
                                                                                                                                                DOMAIN
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-!- SIMILARITY: Contains 1 myosin-like globular head
-!- SIMILARITY: Contains 1 IQ domain.
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"The yeast MYO1 gene e
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MEDLINE=94378003; PubMed=8091229;
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SM00242; MYSC;
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H -> D (IN REF. 1).
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EYTYEGWLSKNK -> NTLWK AGYPKT (IN REF.
MISSING (IN REF. 3).
EKSSSA -> GKNLLVC (IN REF. 1 AND 3).
ENSTITT -> RKFNHHD (IN REF. 3).
E -> R (IN REF. 1 AND 3).
ENTKLFFKAGYLA -> ILTYFQKLEYWS (IN RET. 1 AND 3).
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01-JUL-1993
28-FEB-2003
TISSUE=Brain;
MEDLINE=92366472; PubMed=1323835;
Krueger N.X., Saito H.;
                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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P23471;
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(Rel. 26, Last sequence update)
(Rel. 41, Last annotation update)
osine phosphatase zeta precursor (
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EMBL; X54135; CAA38070.1; -
PIR; A46151; A46151.
HSSP; P18052; 17FO.
Genew; HGNC:9685; PTPRZ1.
MIN; 176891; -
GO; GO:0005887; C:integral
GO; GO:0005001; F:transmemb
GO; GO:0007417; P:central n
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TISSUE=Brain stem;

MEDLINE=93252948; PubMed=8387522;

MEDLINE=93252948; PubMed=8387522;

MEDLINE=93252948; PubMed=8387522;

Levy J.B., Cannil P.D., Silvennoinen O., Barnea G., Morse B.,

Levy J.B., Cannil P.D., Silvennoinen O., Barnea G., Morse B.,

Honegger A.M., Huang J.-T., Cannilzaro L.A., Park S.-H., Druck T.,

Honegger A.M., Huang J.-T., Musacchio J.M., Schlessinger J.;

Consideration of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       brain."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huebner K., Sap J., Ehrlich M., Musacchio J.M., & "The cloning of a receptor-type protein tyrosine expressed in the central nervous system.";
J. Biol. Chem. 268:10573-10581(1993).
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GO:0005887; C:integral to plasma membrane; TAS.
GO:0005001; F:transmembrane receptor protein tyrosine
GO:0007417; P:central nervous system development; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TYPE CARBONIC ANHYDRASE FAMILY. SIMILARITY: Contains 2 protein-tyrosine phospha SIMILARITY: Contains 1 fibronectin type III don CAUTION: CALLED RPTPASE BETA IN REF. 2 AND REF. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISOId=P23471-2; Sequence=VSP 005151;
TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN THE CENTRAL SYSTEM, WHERE IT IS LOCALIZED IN THE PURKINJE CELL LAYER CEREBELLUM, THE DENTATE GYRUS, AND THE SUBEPENDYMAL LAYER
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CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type I membrane ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine + phosphate.
SUBUNIT: THE CARBONIC-ANHYDRASE LIKE DOMAIN BINDS
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Natl. Acad. Sci. U c a company of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
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                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long as and this statement is not removed. I requires a license agreement (See htt an email to license@isb-sib.ch).
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PROSITE; PS50056; TYR PHOSPHATASE 2; 2.

PROSITE; PS50055; TYR PHOSPHATASE PTP; 2.

Signal; Glycoprotein; Transmembrane; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0006470; P:protein amino InterPro; IPR001148; Euk COanhd. InterPro; IPR003961; FN_III.
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InterPro; IPR003961; FN III.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000242; Tyr_PP.
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994
                                                                         Similarity
               GKYYVYLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVAL----
                                VGVTYQGSLFSGPSHI---
                                                 1K1TDQGYVTSHGDHYHYYNGKVPYDA11SEELLMKDPNYKLKDED1VNEVKGGYV1KVD
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AA; 2
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134
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                                                                         3.4%;
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O-LINKED (XYL.
(POTENTIAL).
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N-LINKED
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                                                                         Score 141.5;
Pred. No. 10;
                                                                                                                                  N-LINKED (GLCNAC. . N-LINKED (GLCNAC. .
                                                                                                                                                                                                                                     N-LINKED (GLCNAC.
O-LINKED (XYL.
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PROTEIN TYROSINE PHOSPHAT
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                    N-LINKED
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                                                                  Mismatches
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(GLCNAC.)
(GLCNAC.)
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RESULT 25
NUM1_YEAST
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000402;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence up
01-OCT-1996 (Rel. 34, Last annotation
SEQUENCE FROM N.A.
STRALR-ATCC 28383 / FL100;
MEDLINE=92079907; PubMed=1745235;
Kormanec J., Schaaff-Gerstenschlaeger I.,
Perecko D., Kuentzel H.;
                                                                                                     Saccharomyces cerevisiae (Baker's yeas:
Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                        Nuclear migration protein NUM1. NUM1 OR YDR150W.
                                                                                         NCBI_TaxID=4932;
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                                                                                                       Saccharomycotina; Saccharomycetes; cetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nuclear migration in Saccharomyces cerevisiae is controlled by highly repetitive 313 kDa NUM1 protein.";
Mol. Gen. Genet. 230:277-287(1991).
-i- FUNCTION: CONTROLS NUCLEAR MIGRATION. NUM1 SPECIFICALLY CONTROLS NUCLEAR MIGRATION. NUM1 SPECIFICALLY CONTRESECTION OF THE SUD NECK CYTOSKELETON WITH THE PREDIVISIONAL GZ NUCLEUS PERHAPS BY RECOGNIZING GZ-SPECIFIC CYTOPLASMIC MICROTUBULI OR OTHER COMPONENTS OF THE NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00169; PH; 1. SMART; SM00233; PH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X61236; CAA43554.1;
SGD; S0002557; NUM1.
InterPro; IPR001849; PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: ADDITIONAL REGIONS OF LOWER HC
CONSENSUS (ALMAYS STARTING WITH PROLINE) ARE
FLANKING DOMAINS OF THE TANDEM REPEATS.
SIMILARITY: Contains 1 PH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 PH domain. CAUTION: IT IS UNCERTAIN WHETHER MET-1 IS THE INITIATOR
   1013 YEDLVKCKENPDMEFLKEKSAKLGHTVVSN---EAYSELEKKLEQPSLEYLVEHAKATNH
                               346
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                              -----PEQPSPQPTPEPSP--GPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISR
                                                                                            ---ITSRTAR-GVAVPHGDHYHFIPYSQMSELEERIAR----IIPLRYRSNHWVPDSR
                                                                                                                                                                                                                                                   ENPDMEFLKEKSAKLGHTVVSNEAYSELEKK-------LEQPSLAYLVEHA
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Pred. No. 13;
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                                                              SELEKKLEOPSLEYLVEHAKATNHHLLSDSA
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                                                                            SUBUNIT: MAY FORM PART OF THE CAP-BINDING PROTEIN COMPLEX.
                                                                                                               FUNCTION: INTERACTS WITH THE MRNA CAP STRUCTURE, M7GPPPX. INTERACTION IS REQUIRED FOR EFFICIENT RIBOSOME BINDING TO MRNA. TIF4632 IS PROBABLY ESSENTIAL WHEN TIF4631 IS MISSI
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Initiation factor; Protein biosynthesis;
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ETAPLVPSANRWIPKSRVKKTEKKLAPDGKTELFDKEEVERKMKSLLNKLTLEMFDSIS
                              --- PEVPQVETEKVEAQLKEAEVILAKVTDSSL---KANATETLAGLRNNLTLQIMDNNS
                                                                 TSSSRVSSKRRSKRMGDDR-RSNRGY-----TSRKDRE-----
                                                                                              TLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAE
                                                                                                                              YGPTFLLQFKDKLKFRPDPAWVEAVSSKIVIPPHIARNKPKDSGRFGGDFRSPSMRGMDH
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19.7%; Pred. No.
                                                                                                                                                              ----VEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPN----GY
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RESULT 27 SPT7_YEAST

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SPT7 YEAST
P35177;
01-FEB-1994
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SGD; S0000285; SPT7.
GG; GO:000124; C:SAGA complex; IDA.
InterPro; IPR001487; Bromodomain.
Pfam; PF00439; bromodomain; 1.
PFINITS; PR00503; BROMODOMAIN.
SNART; SM00297; BROMO; 1.
PROSITE; PS0063; BROMODOMAIN 1; 1.
PROSITE; PS0064; BROMODOMAIN 2; 1.
Transcription regulation; NucTear protein; Activator; Bromodomain.
DOMAIN 458 528 BROMODOMAIN.
SEQUENCE 1332 AA; 152616 MW; 083B63624669244F CRC64;
                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95229044; PubMed=7713415;
Gansheroff L.J., Dollard C., Tan P., Winston F.;
"The Saccharomyces cerevisiae SPT7 gene encodes
important for transcription in vivo.";
Genetics 139:523-536(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcriptional activator SPT7.

SPT7 OR YBR081C OR YBR0739.
Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccl
Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                  PIR; S41552; S41552.
                                                                                                                                                                           EMBL; L22537; AAC37424.1; -.
EMBL; X76294; CAA53940.1; -.
EMBL; Z35950; CAA85026.1; -.
EMBL; M87651; AAA35087.1; -.
                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=S288c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence analysis of a 31 kb DNA for Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steensma H.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-S288c
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01-FEB-1994 (Rel.
01-OCT-1996 (Rel.
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ard C., Winston
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1., Barthe C., Doignon F.,
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KEQKALESYRQKIEQNSIMKNGFGTVLKQEDDDQLQFHNDHSL
                          KEAEVLLA--
                                                    DDLEISVWKTVTAKVRAEICLKRTEYFKNGKLNSDSEAFLKNPQRMK---
                                                                                  ED-----
                                                                                                          ----DADAAKKDTEDGLQDKTAENKEAGENNEEEEDDDDEDEDEDMVDSQSYLLEKDDDR
                                                                                                                                                                                                                                              DIISDEGDAYVTPHMGHSHWIGKDS--LSDKEK---VAAQAYTKEKGILPPSPDADVKAN
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                          -KVTDSSLKANATETLAGLRNNLTLQIMDNNSI
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MEDLINE-89385998; PubMed=2780297;

MEDLINE-89385998; PubMed=2780297;

Fuerst P., Moesch H.-U., Solioz M.;

"A protein of unusual composition from Enterococcus

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                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
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MEDLINE=9193128; PubMed=1985895;

Kallunki T., Ikonen J., Chow L.T., Kallunki P.

Kaltructure of the human laminin B2 chain gene divergence from the laminin B1 chain gene.";

J. Biol. Chem. 266:221-228(1991).
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Mammalia; Eutheria;
                                                                                                                                                                                                            or send an email to license@isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Endothelial
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MEDLINE=88198245; PubMed=3360804;
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"Differences in human laminin B2 sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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LAMC1 OR LAMB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1282-1609 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comprising one long and three short arms with globules at end.

THE GAMMA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ), LAMININ-2 (MEROSIN), LAMININ-3 (S-LAMININ), LAMININ-4 (S-LAMININ-6 (K-LAMININ) AND LAMININ-7 (KS-LAMININ).

SUBCELLULAR LOCATION: Extracellular.

TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOI COMPONENT).

DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO DOMAIN: THE ALPHA-HELICAL DOMAINS I AND IN THE BASEMENT MEMBRANES (MAJOI COMPONENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq. 1:275-277(1991).

FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration, and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.

SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bour to each other by disulfide bonds into a cross-shaped molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WITH OTHER LAMININ CHAINS TO FORM A COILED COIL S
DOWAIN: DOMAINS VI AND IV ARE GLOBULAR.
SIMILARITY: Contains 1 laminin N-terminal domain.
SIMILARITY: Contains 11 laminin EGF-like domains.
SIMILARITY: Contains 1 laminin IV domain.
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MIM; 150290; -. C:basement membrane; TAS.

GO; GO:00075604; C:basement membrane; TAS.

R GO; GO:0007492; P:endoderm development; TAS.

R GO; GO:0006461; P:protein complex assembly; TAS.

R InterPro; IPR000204; Laminin_B.

R InterPro; IPR000344; Laminin_EGF.

R InterPro; IPR000345; Laminin_EGF.

R InterPro; IPR000349; Laminin_EGF.

R InterPro; IPR00034; Laminin_B.

R Ffam; PF00052; laminin_Nterm; 1.

DR Pfam; PF00053; laminin_Nterm; 1.

PR PF00055; laminin_Nterm; 1.

R Pr00055; laminin_Nterm; 1.

R Pr00070003; LamB; 1.

R PR00171; SM00180; EGF_Lam; 8.

DR SMART; SM00180; EGF_Lam; 8.

R SMART; SM00186; LamB; 1.

DR SMART; SM00186; EGF_2; 2.

DR RROSITE; PS01036; EGF_1; 8.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01186; EGF_2; 2.

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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
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-!- FUNCTION: Has a role in the initiation
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 Saccharomyces cerevisiae
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[5]
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SNF2 OR SWIZ OR GAM1 OR TYE3 OR RIC1 OR YOR290C.
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"The GAM1/SNF2 gene of Sacc
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                                                                                                                                                                                           cerevisiae.";
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     DOMAIN

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Yeast 13:479-482(1997).
                                                                                                                                                                                                                                               PRINTS; PR00929; ATHOOK.
PRINTS; PR00503; BROMODOMAIN.
SMART; SM00384; AT hook; 2.
SMART; SM00297; BROMO; 1.
SMART; SM00487; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                        Pfam; PF00439; bromodomain; 1.
Pfam; PF00271; helicase C; 1.
Pfam; PF00176; SNF2 N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of licinformatics and the EN the European Bioinformatics Institute. There are no restrue by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence and analysis of a 36.2 kb fragment from the right arm of yeast chromosome XV reveals 19 open reading frames including SNF2 (5 and 1 CDN1 STV41 a putative transport ATPase, a putative ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Poirey R., Cziepluch C.,
Jauniaux J.-C.;
                                                                                                                                                      Bromodomain;
                                                                                                                                                                          Transcription
                                                                                                                                                                                         PROSITE; PS00633; BROMODOMAIN_1; 1.
PROSITE; PS50014; BROMODOMAIN_2; 1.
                                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000330; SNF2_Pfam; PF02178; AT_hook; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWI2/SNF2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Richmond E., Peterson C.L.; "Functional analysis of the DNA-stimulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97025355; PubMed=8871545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97298310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-309 FROM N.A. STRAIN=S288C / FY1679;
                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSF!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: STRONG, TO DROSOPHILA BRAHMA.
SIMILARITY: Contains 1 bromodomain.
SIMILARITY: Contains 3 A.T book DNA-binding repeats.
SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M61703; AAA35059.1;
X57837; CAAA0969.1;
D90459; BAA14423.1;
X89633; CAA61793.1;
X89633; CAA61793.1;
Z75198; CAA99517.1;
Z75199; CAA99519.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: INVOLVED IN TRANSCRIPTIONAL ACTIVATION. THE SWI/SNF COMPLEX IS REQUIRED FOR THE INDUCED EXPRESSION OF A LARGE NUMBER OF GENES. THIS COMPLEX ALTERS CHROMATIN STRUCTURE TO FACILITATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING OF GENE-SPECIFIC I SUBUNIT: COMPONENT OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S15047; S15
SFAC; T02401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S0005816; SNF2
                                                                                                                                                                                                                                 SM00490; HELICC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000637;
   1446
1502
1502
1568
                                                                                            1; ATP-binding;
55 68
207 239
792 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S15047
                                                                                                                                                                        regulation;
   68
239
799
897
1456
1513
1526
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uch C., Tobiasch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AT hook.
Bromodomain.
DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                       SNF2_N.
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                                                                                                                                                        Helicase
                                                                                                                                                                          Nuclear protein;
                       A.T HOOK
A.T HOOK
A.T HOOK
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E SWI/SNF GLOBAL
     BROMODOMAIN
                                                                                              ALA/GLN-RICH.
ATP (BY SIMILARITY)
                                                                                                                                      GLN-RICH
                                                                               BOX
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(H)
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                                                                                                                                                                          Activator;
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                                                                                                                                                                          Repeat;
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MBL outstation -
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Query Match
Best Local
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                                                    Merozoite
(PMMSA) (P
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                       (P195)
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                                                                                                                                                                                                                            QTNAFL-DSLTRAVKDQQKYTKE
                                                                                                                                                                                                                                                               ETLAGLRNNLTLQIMDNNSIMAE
                                                                                                                                                                                                                                                                                                                                                                           SKIRNINVQDALLTNQLYKNHELLKLERKKTEAVARLKSMNKSAINQYNRRQDKKNKRLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q----KPVPLNVLQDQYKEGIKVVDIDDPDMMV---DSFTMPNISHSN-IDYQTLLANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VHNAKNGTLDKNSQTVSGTPITQ---TESKKEENETISNVAKTAPNSNKTHTEQNNPPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAP---ITHPERLGKPNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKEN---VAPRDQEFYDKAYNLLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSLSEFARRRQPTDQNNQSNLNGGNNTQQPGTNSHYNNTNTDNVSGLTRNA------
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                                                                                                                                                                                                                                                                                                  FGHRLIATHTNLERDEQKRAEKKAKERLQALKANDEEAYIK----LLDQTKDTRITHLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLDKLLNDECTESTRENALY---DYYALQLLPLQKAVRGHVLQFEWHQNSLLTNTHPNFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---PYMVEHTVEVKNGNLIIPHKDHY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHAK-----FTIEPGVLPVGIDT------HTATDIYQ-----TLIALNLDTTVND
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                                  87 (Rel. 05, Created)
96 (Rel. 33, Last sequence update)
03 (Rel. 42, Last annotation update)
surface protein 1 precursor (Merozoite
                                                                                                                                                                                                                                                                                                                                                                                                                ----GYTLEDLFATIKYYVEH-----PDERPHSNDGWGNASEHVLGKKDHSED-PNK---
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                                                                                                                                   STANDARD;
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Pred. No. 9.
                                                                                                                                   PRT;
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                                      surface antigens)
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Bukaryota; Alveolata; Apicomplexa; Haemosporida;
NCBI_TaxID=5848;
[1]
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Holder A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Primary structure of the precursor to the three antigens of Plasmodium falciparum merozoites."; Nature 317:270-273(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=86014355; PubMed=2995820;
Holder A.A., Lockyer M.J., Odink
Nicholls S.C., Hillman Y., Davey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
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                                                                                            SELEERIARIIP-LRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNS-SLVSQ
                                                                                                                                 ADLKHRVRNYLLTIKELKYPQ
                                                                                                                                                                ASQSNDIDSLLKQLYKLELSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQM
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USO1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USO1_YEAST
P25386;
01-MAY-1992
                                                                                                                                       Submitted
                                                                                                                                                                                      Submitted (FEB-1993) to the
                                                                                                                                                                                                              SEQUENCE OF 782-1790 FROM N.A. Hostetter M.K., Herman D.J., B
                                                                                                                                                                                                                                                    "A cytoskeleton-related gene, uso1, is required protein transport in Saccharomyces cerevisiae.", J. Cell Biol. 113:245-260(1991).
                                                                                                                                                                                                                                                                                          Nakajima H., Hirata A.,
Yamasaki M.;
                                                                                                                                                                                                                                                                                                    MEDLINE=91185402; PubMed=2010462;
Nakaiima H., Hirata A., Ogawa Y.,
                                                                                                                                                                                                                                                                                                                              STRAIN=X2180-1A;
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; /
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
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16-OCT-2001 (Rel. 40, Le
Intracellular protein to
USO1 OR INT1 OR YDL058W
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                                                                                                                                                                                                    Kendrick K.E.;
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                                 MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE ER AND THE GOLGI COMPLEX.

ER AND THE GOLGI COMPLEX.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL COLLED COLLS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.
                       SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C
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SWISS-PROT entry is copyright. It is produced through a collaboration
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Symington L.S.;
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Pfam; PF04871; Usol_p115_C; 1.
Pfam; PF04897; Usol_p115_C; 1.
Transport; Protein Franchised; 1.
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             EDLAAQLK--KYEEQIA--NKERQYNEE---ISQLNDEITSTQ----QENESIKKKNDEL 1203
                                   DDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDBHDIISDEGDAY
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                                                                                    TAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLV 485
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Bioinformatics Institute. There are no restrictions
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutcon G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Belson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Bobrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mount S.M., Moy M., Murbhy B., Murbhy L., Murry D.M., Nelson D.,
RA Mount S.M., Moy M., Murbhy B., Murbhy L., Murry D.M., Nelson D.I.,
RA Mount S.M., Moy M., Murbhy B., Murbhy L., Murry D.M., Nelson D.I.,
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Merkulov G., Milshina N.V., MUDGLLY V., MUZDY D.M., Nels Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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Neoptera; Endopterygota; Diptera; Brachycera;
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era; Muscomorpha;
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HOMEOBOX. ALA/GLN-RICH

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Homeobox;

PROSITE; PS00027; PROSITE; PS50071;

regulation;

7; HÓMEOBOX 1; 1.
1; HOMEOBOX 2; 1.
2; 1.
egulation; Homeobox; DNA-binding;
egulation; Homeobox; DNA-binding;
cottain; Nuclear protein; Repeat; Coile;
coiled COIL (POTENTIAL).
343
COILED COIL (POTENTIAL).
964
CUT 1.
1161
COILED COIL (POTENTIAL).

Coiled

coil

Pfam; PF00046; homeobox; 1.

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235 271 384 547 616

ASP/GLU-RICH ASP/GLU-RICH ALA-RICH. HIS/GLN-RICH

ASN-RICH. ASP/GLU-RICH ALA-RICH.

(ACIDIC)

ALA-RICH

(OPA-REPEAT) (ACIDIC). (ACIDIC)

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Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarnan D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I. Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2155(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0008587; P:wing margin morphogenesis; NAS InterPro; IPR007108; Cut homeo. InterPro; IPR00350; Homeo CUT. InterPro; IPR001356; HomeoDox.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Base; FBgn0004198; ct.
GO:0005634; C:nucleus; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXPRESSED DURING EMBRYONIC DEVELOPMENT.

DOMAIN: ASN AT POSITION 47 OF THE HOMEOBOX MAY REGULATING DNA-BINDING ACTIVITY BY PROMOTING HO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear (Probable).
TISSUB SPECIFICITY: Detected in many cells in the central nervous system, all external sensory organs, some peripheral neurons, and in the non-neural cells of the spiracles and the Malpighian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE: CELL-SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Specifically, functions as a determination factor that specifies sensory organ identity in precursor cells. Probably also involved in cell type specification of Malpighian tubules. In absence of cut gene external sensory organs are transformed into chordotonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Regulator of cell fate decisions in multiple lineages Specifically, functions as a determination factor that specifies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HETERODIMERIZATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the Swiss Institute of Bioinf
pean Bioinformatics Institute.
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CUT HOMEOBOX FAMILY
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DOMAIN
SEQUENCE
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P15205; Q62958; Q9ERZ1; Q9QW92;
01-APR-1990 (Rel. 14, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                          SEQUENCE OF 1-142 FROM N.A.
STRAIN-Sprague-Dawley; TISSUE=Testis;
MEDLINE=96257242; PubMed=8666295;
                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                            Microtubule-associated
                                                                                                                                                                                                                    Rattus norvegicus (Rat).
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thi; Muridae; Murinae; Rat
  of.
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MAD., Nothias F., Boyne L.J., Fischer I.;

"Differential regulation of microcubule-associated protein 1B (MAP1B)
in rat CNS and PNS during development.";

J. Neurosci. Res. 49:319-332(1997).

-!- FUNCTION: The function of brain MAPS is essentially unknown.
Phosphorylated MAP1B may play a role in the cytoskeletal changes
that accompany neurite extension. Possibly MAP1B Binds to at least
two tubulin subunits in the polymer, and this bridging of subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J.,
Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H
"Neuraxin, a novel putative structural protein of the rat cent
nervous system that is immunologically related to microtubule-
associated protein 5.";
EMBO J. 8:2879-2888(1989).
                                                                                                                                                            EMBL; U52950; AAB17068.1;
EMBL; X60370; CAC16162.1;
EMBL; X16623; CAA34620.1;
PIR; A56577; A56577.
                    Microtubules; Repeat; Phosphorylation.
CHAIN 2 2459 MAP1 LIGHT
                                                                                                     InterPro; IPR000102; MAP1B_neuraxin. Pfam; PF00414; MAP1B_neuraxin; 10.
                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as modified and this statement is not removed. I
                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBUNIT: 3 different light chains, LC1, LC2 with MAP1A and MAP1B proteins.
-i- TISSUE SPECIFICITY: Nervous system (spinal cerebellum and cerebrum). Not expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE, AND PHOSPHORYLATION MEDLINE=97405699; PubMed=9260743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90059871;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Sprague-Dawley; TISSUE=Bra
MEDLINE=92347374; PubMed=1639092;
                                                                                                                                                                                                                                                                                                          or send
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Gene 172:307-308(1996).
                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: riuspins, To MAPIA.
SIMILARITY: TO MAPIA fragment of this protein (resincation: A C-terminal fragment of this protein (resincation: A C-terminal described as neuraxin in Ref. 3. 2459) was originally described as neuraxin in ref. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nerve levels are high early in development but decrease during postnatal development and are low in adults. In dorsal root ganglia levels remain high throughout development. InDUCTION: By nerve growth factor.

INDUCTION: By nerve growth factor.

IOMANN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAP1B to microtubules.

PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated from MAP1B by proteolytic processing. It is free to associate with both MAP1A and MAP1B. It interacts with the amino-terminal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of MAP1B (By similarity).
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                                                                                                                                                                                                                                                                                                       s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF 96-2459 FROM N.A., DOMAIN prague-Dawley; TISSUE=Brain,
                                                                              PS00230; MAPIB_NEURAXIN; 8.
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         NGYTLEDLFATIKYYVEHPDERPHSNDG------WGNASEHVLGKKDHSEDPNKNFK 704
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RESULT
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                                                                                                Pfam; PF00373; Band 41; 1.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00935; BAND41.
PRINTS; PR00905; PRTYPHPHTASE.
SMART; SM00295; B41; 1.
SMART; SM00194; PTPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTNL MOUSE
Q62136;
Q1-NOV-1997
                                                                                                                                                                                HSSP; P29350; 1GWZ.
MGD; MGI:134406; Ptpn21.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000387; TYR_phosphatase:
InterPro; IPR000242; Tyr_pp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oncogene 10:407-414(1995).

-!- FUNCTION: MAY BE INVOLVED IN THE REGULATION
-!- DIFFERENTIATION OF LIVER CELLS.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate.
-!- TISSUE SPECIFICITY: LIVER.
PROSITE; PS00660; FERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS00061; FERM 3; 1.
PROSITE; PS00033; TYR_PHOSPHATASE_PTP; 1.
PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
PROSITE; PS00055; TYR_PHOSPHATASE_2; 1.
Structural protein; Cytoskeleton; Hydrolase
                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE=95140431; PubMed=7838537;
Higashitsuji H., Arii S., Furutani M., Imamura M., Kaneko Y.,
Takenawa J., Nakayama H., Fujita J.;
"Enhanced expression of multiple protein tyrosine phosphatases in the
regenerating mouse liver: isolation of PTP-RLIO, a novel cytoplasmic-
type phosphatase with sequence homology to cytoskeletal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
TISSUE=Liver;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                          EMBL; D37801; BAA07053.1; PIR; I58345; I58345.
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Sciurognathi;
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chi; Muridae;
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YIS3_YEAST
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AC P4056
DT 01-FE
DT 15-SE
DT 15-SE
DE HYPOT
GN YIROG
OC Sacch
OC Sacch
OX NCBI
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Matches 137
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01-FEB-1995 (Rel. 31, 1
15-SEP-2003 (Rel. 42, 1
Hypothetical 74.8 kDa F
YIROOW OR YIB3W.
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01-FEB-1995
01-FEB-1995
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ACT SITE
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              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycosaccharomycetales; Saccharomycetaceae; Saccharomycetaceae; Saccharomycetaceae; Saccharomycetaceae;
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Pred. No. 7.2;
90; Mismatches
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MW; 529F
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PROTEIN-TYROSINE PHOSPHATASE.
BY SIMILARITY.

POLY-PRO.
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BET1-PAN1 in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X79743; -; NOT ANNOTATED_CDS.
EMBL; Z38062; CAA8625:1; -.
PIR; Z380437; S48437.
SGD; S0001442; Y1R003W.
Hypothetical protein.
SEQUENCE 679 AA; 74763 MW; 9DET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95282515; PubMed=7762303;
Voss H., Tamames J., Teodoru C., Valencia A.,
Schwager C., Zimmermann J., Sander C., Ansorge
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SEQUENCE FROM N.A.
STRAIN=S288C;
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   ---DIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPP---
                                                                   LAFLAPITHPERLG-----KPNSQIEYTEDEVRIAQLADKY----
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                                     ----PSERPKRRAPPPVPKKPSSRIAAFQEMLQKQQQQDLHNNGNSSATTASADIAKKH
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7; Mismatches 260;
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"Molecular characterization and expression of a Staphylococcus aureus collagen adhesin.";
J. Biol. Chem. 267:4766-4772(1992).
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                                                                                                              Moore D., Jin L., Schneider A., Del
Narayana S.V.L.;
"Structure of the collagen-binding
                                                                                                                                            MEDLINE=97475225; PubMed=9334749;
Symersky J., Patti J.M., Carson M
                                                                                                                                                                                 MEDLINE=94032261; PubMed=8218209; PALTLI J.M., Boles J.O., Hoeoek M.; Patti J.M., Boles J.O., Hoeoek M.; "Identification and biochemical characterization of the ligand binding domain of the collagen adhesin from Staphylococcus aura Biochemistry 32:11428-11435(1993).
                                                                                                                                                                                                                                   STRAIN=FDA
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MEDLINE=92165839; PubMed=1311320;
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15-DEC-1998
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15-SEP-2003
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European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
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(Rel. 37, Last sequence update)
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InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR006192; LPXTG.
TIGRRAMS; TIGR01167; LPXTG anchor; 1
PROSITE; PS50847; GRAM_POS_ANCHORING; FALSE NEG.
Cell wall; Peptidoglycan-anchor; Repeat; Signal;
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                                     GNLSNSRTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLY
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01-OCT-1996 (Rel.
                                                                             "Polymorphism of the precursor for the Plasmodium falciparum merozoites: studi
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Stunnenberg H., Bujard H.;
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Eukaryota; Alveolata;
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Pred. No. 13;
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YKLPLSQRHVESD

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79

137

Gaps

29

-VG--

EGYVFEEK

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442

284

192

-PNTL

561 331 501

LSG

359

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RESULT 40
BUD3 YEAST STANDARD; PRT; 1636
AC P2558; P2557; P87007;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1995 (Rel. 32, Last sequence updated)
DT 01-MOV-1995 (Rel. 41, Last sequence updated)
DT 28-FEB-2003 (Rel. 41, Last sequence updated)
DT 28-FEB-2003 (Rel. 41, Last sequence updated)
DT 28-FEB-2003 (Rel. 41, Last sequence updated)
DT 28-FEB-2003 (Rel. 41, Last sequence updated)
DT 28-FEB-2003 (Rel. 41, Last sequence updated)
DT 28-FEB-2003 (Rel. 41, Last sequence updated)
DT 28-FEB-2003 (Rel. 41, Last sequence updated)
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DT 28-FEB-2003 (Rel. 41, Last sequence updated)
DT 28-FEB-2003 (Rel. 41, Last sequence updated)
DT 28-FEB-2003 (Rel. 41, Last sequence updated)
DS SCCCHAromycetalses; Saccharomycetalses;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ś
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                                                                                                                                                                                                         the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entities requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=95247824; PubMed=7730410;

Chant J., Mischke M., Mitchell B., Herskowitz I., Pringole of Bud3p in producing the axial budding pattern J. Cell Biol. 129:767-778 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                        mitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. FUNCTION: CO-ASSEMBLES WITH BUD4 AT BUD SITES. BUD4 AND BUD3 M COOPERATE TO RECOGNIZE A SPATIAL LANDMARK (THE NECK FILAMENTS) DURING MITOSIS AND THEY SUBSEQUENTLY BECOME A LANDMARK FOR ESTABLISHING THE AXIAL BUDDING PATTERN IN G1.
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AC P06546
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DT 01-OCT
DT 28-FEB
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28-FEB-2003
Middle cell
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P06546;
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Query Match
Best Local
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AFGNTSMSTDNMKISSDLSSNKTVLGNAQKV
                                                                                                                                                SDISFT-YDTHNNDEPDKRLMELKPPS---QDEIPDDRFYT
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                                 NATETLAGLEN-NLTLQIMDNNSIMAEAEKL
                                                                                                       DPNKNFKADEEPVEETPAEPEVPQVET---EKVEAQLKEAEV---
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(Rel. 06, Created)
(Rel. 12, Last sequence update)
(Rel. 41, Last annotation updat
wall protein precursor (MWP).

on update)

STANDARD;

1053

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EMBL; M15364; AAA87321.1; -.
EMBL; M14238; AAA22372.1; -.
EMBL; M19115; AAA22760.1; -.
EMBL; M31828; AAA22760.1; -.
PIR; A28555; A28555.
InterPro; IPR001119; SLH.
Pfam; PF00395; SLH; 2.
PROSITE; PS01072; SLH DOMAIN; 2
CCell wall; S-layer; SIgnal; RepSIGNAL 1 23
CHAIN 24 1053
CHAIN 29 92
DOMAIN 29 92
SLI
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between
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Tsuboi A., Uchihi R., Adachi T., Sasaki T., Hayakawa S., Yam Tsubagoshi N., Udaka S.;
Tsukagoshi N., Udaka S.;
"Characterization of the genes for the hexagonally arranged layer proteins in protein-producing Bacillus brevis 47: comp nucleotide sequence of the middle wall protein gene.";
J. Bacteriol. 170:935-945(1988).
                                                                                                                                                                                                                                                                                                     protein gene from Bacillus brevis 47.";

J. Bacteriol. 171:6747-6752(1989).

-!- FUNCTION: THE MIDDLE WALL PROTEIN BINDS TO PEPTIDOGLYCAN AND THE OUTER CELL WALL PROTEIN.

-!- SUBUNIT: THE MIDDLE CELL WALL LAYER IS COMPOSED OF SUBUNITS THE MIDDLE CELL WALL PROTEIN. THESE PROTEINS FORM A HEXAGOND ARRAY WITH A LATTICE CONSTANT OF 14.5 NM IN THE MIDDLE CELL ARRAY WITH A LATTICE CONSTANT OF 14.5 NM IN THE MIDDLE CELL
                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                      "In vitro reconstitution of a hexagonal array with protein synthesized by Bacillus subtilis harboring
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90078123; PubMed
Tsuboi A., Uchihi R., En
Tsukagoshi N., Udaka S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-50 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamagata H., Tsukagoshi N., Udaka S.; "Characterization of the genes coding for two major cell wall proteins from protein-producing Bacillus brevis 47: complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=87008404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Tsukagoshi N.,
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Bacteria; Firmicutes; Bacillales; Paenibacillaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and
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Bioinformatics Institute.
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R., Engelhardt H.,
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                                                                PVKLYRAT
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                                                                                                PNKNFKADEEPVEETPAEPEVPQVE----TEKVEAQL---KEAEVLLA----
                                                                                                                                                                                                                               -EVKNGNLIIPHKDHYHNIKFA-----WFD-----
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                                                                ELNSKVKAE-DVDAIEFYFNGKKVEPSLLNFKDGVITIGYNTEDKVTSSKI
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Pred. No. 7.
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Pfam; PF01576; Myosin_N; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; Myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096. TO
                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
             NP_BIND
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                           EMBL; AB022023; BAA36494.1; -. EMBL; U15716; AAA87715.1; -. HSSP; P10587; 1BR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 270:14533-14540(1995).

-!- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKIN CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND CAPPING (BY SIMILARITY).

-!- SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 H CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) A REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHO CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPE CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
-!- SIMILARITY: Contains 1 myosin-like globular head domain.
-!- SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Neuronal cell expression of inserted isoforms myosin heavy chain II-B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohara M., Ishiguro N., Shinagawa M.; "Bos taurus nonmuscle myosin heavy chain B mRNA, complet Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, nonmuscle type B (Cellular myosin
type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B).
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                                                                    DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
 SEQUENCE
                                                                                                                                                                                                                                          Pfam; PF00612; IQ; 1
                                                                                                                                                                                                                                                                    interPro;
                                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                              nterPro; IPR000048;
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                                                                                                                                                                                                            PF00063; myosin_head; 1.
PF02736; Myosin_N; 1.
                                                                                                          PS50096; IQ; 1.
ATP-binding; Calmodulin-binding;
                                                                                                                                                                                                                                                                 IPR001609; myosin_head.
IPR004009; Myosin_N.
IPR002928; Myosin_tail.
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Eutheria; Cetartiodactyla;
786
845
178
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1976
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                                                                                                Alkylation;
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           ALKYLATION (SH-1) (POTENTIAL). ALKYLATION (SH-2) (POTENTIAL).
                                      IQ.
COILED COIL (POTENTIAL)
ATP (POTENTIAL)
                                                                                 MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Eutei
actyla; Ruminantia; Pecora;
 6144354451C0F790
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                                                                                                             Actin-binding;
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AS SECRETION AND
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AND 2
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CSPG2

Mus musculus (Mouse)

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DT 15
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Best Local Similarity
Matches 152; Conserv
                          PROUSE STANDARD; PRT; 3358 AA.

PRGCV MOUSE STANDARD; PRT; 3358 AA.

Q62059; Q62058; Q9CUU0;

Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M).
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18.5%; Pred. No. 18;
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peeole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peeole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
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J. Biol. (
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                                                                                                                                                                                                                                                                                                                                                                       Aspberg A., Adam S., Kostka G., Timpl Fibulin-1 is a ligand for the C-type
                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=10400671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-1692 FROM N.A. STRAIN=C57BL/6J; TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95181355; PubMed=7876137; Zako M., Shinomura T., Ujita M., Ito "Expression of PG-M(V3), an alternati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION WITH FBLN1
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Biol.
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                                                                                                                                                                                                                                   SUBCELLULAR LOCATION:
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=4;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                   SUBUNIT:
                                                                                                                                                                                                                                                                                             the regulation of cell motility,
                                                                                                                                                                                                                                                                                                           FUNCTION: May play a role in intercellular signaling and connecting cells with the extracellular matrix. May take
                                                                                                                                                                                                                                                                               hyaluronic acid
                                                                                                                                                                          IsoId=Q62059-1;
                                                                                                                                            [soId=Q62059-2;
                                                                                                                                                                                                                                                                                                                                          Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ninomura T., Zako M., Ujita M., Kimata K., forms of mouse PG-M, a large chondroitin an generated by alternative splicing.";
                                                                                                                                                                                                                                                                   Interacts with
                                                                                                                                                                                                                                                                                                                                            274:20444-20449(1999).
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                                                                                                                                                                          Sequence=Displayed;
                                                                                                                                         Sequence=VSP_003087,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an alternatively
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                   FBLN1.
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                                                                                                                                                                                                                                                                                                                                                                       R., Heinegaard
lectin domains
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Y spliced f
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                                                                                                                                          VSP_003088;
                                                                                                                                                                                                                                                                                               matrix. May take part and differentiation.
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PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS00614; C TYPE LECTIN 2; 1.
PROSITE; PS00022; EGF 1; 2.
PROSITE; PS001186; EGF 2; 1.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS01187; EGF CA; 1.
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Interpro; IPR000742; EGF_2.
Interpro; IPR000742; EGF_1:
Interpro; IPR001881; EGF_1:
Interpro; IPR006209; EGF_1:
Interpro; IPR007110; Ig-1:
Interpro; IPR003599; Ig-
Interpro; IPR003599; Ig-
Interpro; IPR003006; Ig-MHC.
Interpro; IPR003006; Ig-MHC.
Interpro; IPR0030181; Liettin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00409; IG; 1.
SMART; SM00445; LINK; 2.
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Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 1.
Pfam; PF00084; xlink; 2.
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EMBL; D32040; BAA06802.1; -.
EMBL; AK014525; BAB29411.1; -.
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Hyaluronic acid
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MGD; MGI:102889; Cspg2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
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                                                                                                     SHGSSEESLQVQEKYEGAVTLSPTEESFEGSGDALLAGYTQAIYNESVTPNDGK----QA
                                                                                                                                                                            LHHSEYKSSLY-PTS--TLPSTEPYKSPSEGIEDGLQDNIQFEGSTLKPSRRKTTESIII 2522
                                                                                                                                                                                                               SGEGSGEVDTLDLVYTSGTTQASSQGDSMLASHGFLEKHPEVSKTEAGATDVSPTASAMF
                                                                                                                                                                                                                                                  PKTHRPQTMSGLISNENSSASEAEEGATSPTAFLPQTYSVEMTKHFAPSESQPSDLFNVN
                                                  LADKYTTSDGY-IFDEHDIISDEGDAYVTPHMGHSHWIGKDS---
                                                                                                                       KQESVSHTLTAKKE-----NVAPRDQEFYDKAYNLLTEAHKALFX----NKGRNSDFQA
                                                                                                                                         DLDKEDSKDLGLTITESAIVKSLPELTSDKNIIIDIDHTKPVYEYIPGIQTDLDPEIKLE 2582
                                                                                                                                                                                             ----RYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVF
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YVSIGSTYLIAQTLTELPNVVRPSDSTHYTEATPEVSSLAEL-----SPQIPSSPFP--
               ----KEKVAAQAYTKEKGILPPSPDAD-VKANPTGDSAAAIYNRVKGEKRIPLVRLPYM
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A -> G (IN REF. 3).
MISSING (IN REF. 3).
I -> T (IN REF. 3).
TVWNSNS -> QFGIQTA (IN REF.
MW; 071B80026BC0762D CRC64;
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P09790;
01-MAR-1989 ()
01-MAR-1989 ()
28-FEB-2003 ()
IGA-specific
                                                                                                                                                                                                                                                                                                                                         MEDLINE-90154052; PubMed=2105953;
Bachovchin W.W., Plaut A.G., Flentke G.R., Lynch M., Kettner C.A.;
"Inhibition of IgAl proteinases from Neisseria gonorrhoeae and
Hemophilus influenzae by peptide prolyl boronic acids.";
J. Biol. Chem. 265:3738-3743(1990).
-i- FUNCTION: THIS PROTEASE IS SPECIFIC FOR IMMUNOGLOBULIN A.
-i- CATALYTIC ACTIVITY: Cleavage of immunoglobulin A molecules at
certain Pro-[-xaa bonds in the hinge region. No small molecule
                                                                                                                          modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protease).
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MEROPS; S06.001; -.
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                                                                                                                                                                                                     between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
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                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                           SUBSTRATES ARE KNOWN.
SUBCELLULAR LOCATION: Secreted.
SUBCELLULAR LOCATION: Secreted.
DOMAIN: THE SIGNAL PEPTIDE GUIDE THE PRECURSOR TO THE PERIPLAS DOMAIN: THE STANDAL PEPTIDE GUIDE THE PRECURSOR TO THE PROTESSE WITH OUTER MEMBRANE TO FORM A PORE FOR EXCERSION OF THE PROTESSE DOMAIN THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTEOLYSIS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S6.
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                                                                                                                                                         non-profit institutions as long and this statement is not removed.
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(Rel.
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                                                                                                                                          moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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InterPro; IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
InterPro; IPR000710; IGA_S6.
InterPro; IPR004899; PerTactin.
Pfam; PF03797; Autotransporter; 1.

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KADEEPVEETPAEPEVPQVETEKVE
                                                                        MSNTGYGRDYASAQYRRFSSKRTQTQTGIDRSLSENMQIGG---VLTYSDSQHT-----F
                                                                                             ANPTG----DSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWF
                                                                                                                             DKHPQDNTELHEKVE--TAGLQP-----RAAQPRTQAAAQADAVSTNTNSALSDAMASTQ
                                                                                                                                                                                ERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRI----AQLADKYTTSD
                                                                                                                                                                                                                                                                  PAPNLKID-----SNSSL--VSQLVRKVGEGYV--FEEKGISRYVFAKDLPSETVKNL
                                                                                                                                                                                                                                                                                         RKAAELAAKQKAEAERKARELARQ----
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                                 DQAGGK--NTFVQANLYG--KYYL-
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                                                   DDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGK-KDHSEDPNK-NF
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SGD; S0004692; YMR086W.
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Transcription factor 8 (NIL-2-A zinc finger regulator of IL2).
                                                                                                                                                                                                                        expression.";
Science 254:1791-1794(1991)
                                                                                                                                                                                                                                              MEDITINE 22108424; PubMed=1840704; MEDITINE 22108424; PubMed=1840704; Williams T.M., Moolten D., Burlein J., Romano J., Bhaerman F. Godillot A., Mellon M., Rauscher F.J. III, Kant J.A.; "Identification of a zinc finger protein that inhibits IL-2
                                                                                                                                                                                                                                                                                                                                                                         Bachman N.J., "A human zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                Watanabe Y., Kawakami K., Hirayama Y., Nagano K.; "Transcription factors positively and negatively regulating ATPase alpha 1 subunit gene."; J. Biochem. 114:849-855(1993).
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TISSUE SPECIFICITY: EXPRESSED IN HEART AND SKELETAL MUSCLE, B NOT IN LIVER, SPLEEN, OR PANCREAS.
SIMILARITY: BELONGS TO DELTA-EF1/ZFH-1 FAMILY OF TWO-HANDED Z
 European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not remove.
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                                         SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EM
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                                                                                                                                                                                                                                                                                                                           FROM N.A.

N.J., Scarpulla R.C.;

n zinc finger homeodomain protein homologous to '
rvstallin enhancer binding protein, delta EF1.";
rvstallin enhancer binding protein, delta EF1.";
                                                                                                                                                                                                                                                                                                                OF 390-1124 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OKTSKSNS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VETEKVEAQLKEAEVLLAKVTDSSLKANATETLAG-LRNNLTLQIMDNNSIMAEAEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Primates;
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Catarrhini;
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          There are no restrictions ng as its content is in
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i; Hominidae;
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Best Local
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ZN-FING
ZN-FING
ZN-FING
DNA-BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0003713; F:transcription co-activator act:
GO; GO:0003714; F:transcription co-repressor act:
GO; GO:0003700; F:transcription factor activity;
GO; GO:0008270; F:zinc ion binding activity; TAS
GO; GO:0008283; P:cell proliferation; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00028; ZINC_FINGER_C2H2
PROSITE; PS50157; ZINC_FINGER_C2H2
Transcription regulation; DNA-bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000010; Homeobox; 1. 
ProDom; PD000003; Znf C2H2; 2. 
SMART; SM00389; HOX; 1. 
SMART; SM00355; Znf C2H2; 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001356; Homeobox.
InterPro; IPR007087; Znf_C2H2.
Pfam; PF00096; zf-C2H2; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; JX0293; JX0293
TRANSFAC; T00625; -
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EMBL; U12170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:11642; TCF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domeobox;
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 358
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                     DQPQSANANE-
                                                                                                                                                                           NROKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHY
SPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAK----DLPSETVKNLE-
                                                                                     GTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESD-----
                                                                                                                              HYIPKNELSASELAAAEA-----FLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVSNP
                                                                                                                                                                                                  SAISL---
                                                                                                                                                                                                                      SEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHADNVRTKE-----EI 132
                                                                                                                                                                                                                                                                IDGKQATQKTENLTPDEVSK-REGINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAII
                                         SRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEP
                                                               YALNAQPSAEELSKIADSVNLPLDVVKKWFEKMQAGQISVQSSEPSSPEPGKVNIPAKNN
                                                                                                           DL--KQPTQPPPLPAAEAEKPESSV$SATGDGNLSPSQPPLK-
                                                                                                                                                      LTVKSEKDKSFEGGV--NDSTCLLC-----DD------CPGDINALPELKHY
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                                                                                                                                                                                                                                                                                       104;
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V -> I (IN REF. 2).

E -> Q (IN REF. 3).

I -> T (TW
                     PQDSTVNLQS-----PLKMTNSPVLPVGSTTNGSRSSTPSP
                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                             C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE
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Pred. No. 9.2
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Q (IN REF. 3).
T (IN REF. 2).
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S (IN REF. 3).
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6.
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pinding; Repeat.
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                                                                                     -GLVFDPAQIT
                                                                                                           NLLSLLKAY
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Q9JKI1; Q9JK10; Q9ROD9; Q9WUB9; Q9WUF0;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo
(Glut4 vesicle 20 kDa protein).
"Cloning of a member of the reticulon minor splice variants.";
Submitted (FEB-1999) to the EMBL/GenBa
                                                                       STRAIN=Wistar Kyoto;
                                                                                                                                           "Nogo-A is a myelin-associated neurite outgrowth inhibitor and antigen for monoclonal antibody IN-1.";
                                                                                                                                                                               Chen M.S., Huber A.B., Van der Haar M.E., Spillmann A.A., Christ F., Schwab M.E.;
                                                                                                                                                                                                                 MEDLINE=20129258; PubMed=10667796;
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lie
"Cloning and characterization of a 22 kDa protein
a new member of the reticulon family.",
Biochim. Biophys. Acta 1450:68-76(1999).
                                                                                                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley;
MEDLINE=99249816; PubMo
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 3),
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTN4 OR NOGO.
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                                                  Ito T., Schwartz S.M.
                                                                                        SEQUENCE FROM N.A.
                                                                                                                            Nature 403:434-439(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                   _TaxID=10116;
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Q9JK10; Q9ROD9; Q9WUE9; Q9WUF0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --TEGLMKDDRAESQASS-LGQKVGESSEQVSEEKTN 1122
                                                                                                                                                                                                                                                                                                                                               wley; TISSUE=Adipocyte;
PubMed=10231557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKLSKQESVSHTLTAKKE------
                                                                                        (ISOFORMS
                                                                                                                                                                                                                                      (ISOFORMS 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -SYCKREAEERDSTEQEEAGPEILSNEHVGARASPSQGDSDERESLTREED
                                                                   TISSUE=Vascular smooth muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VPCLRALAANKQTILIPQVAYTYSTTVSPAVQEPPLKVI
 EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKKKMRKTENGMYACDLCDKI-FQKSSSLLRHKY--
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                                gene family in rat:
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                                                                                                                                                                                                Frank M.,
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                        Lienhard G.E.;
ein from rat adipocytes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein) (Foocen)
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   TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                       TRANSMEM DOMAIN
                                                                                                                                                                                                                                                                                                                                                                              EMBL; APO51335; AAF01564.1; -.
EMBL; AJ242961; CAB71027.1; -.
EMBL; AJ242963; CAB71029.1; -.
EMBL; AJ242963; CAB71029.1; -.
EMBL; AF132045; AAD31019.1; -.
EMBL; AF132046; AAD31020.1; -.
EMBL; AF132046; C:nuclear membrane; intrinsic p.
GO; GO:0030176; C:sendoplasmic reticulum membrane, intrinsic p.
GO; GO:0005635; C:nuclear membrane; ISS.
GO; GO:00056315; F:protein binding activity; ISS.
GO; GO:001987; P:negative regulation of anti-apoptosis; ISS.
GO; GO:0030517; P:negative regulation of axon extension; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GrandPre T., Li S., Strittmatter S.M. "Nogo-66 receptor antagonist peptide Nature 417:547-551(2002).
 VARSPLIC
                                 VARSPLIC
                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                           Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02453; Reticulon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22033691; PubMed=12037567; GrandPre T., Li S., Strittmatter S.M.;
                                                                                                                            /ARSPLIC
                                                                                                                                             DOMAIN
                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are present in dorsal root ganglion, sciattic nerve and PC12 cells after longer exposure. Isoforms 2 and 3 are detected in kidney, cartilage, skin, lung and spleen. Isoform 3 is expressed at high level in skeletal muscle. In adult animals isoform 1 is expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=1; Synonyms=Nogo-A, NI-220-250; IsoId=Q9JK11-1; Sequence=Displayed; Name=2; Synonyms=Nogo-B, Foocen-M1; IsoId=Q9JK11-2; Sequence=VSP 005658; IsoId=Q9JK11-2; Sequence=VSP 005658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=4; Synonyms=Foocen-M2;
IsoId=Q9JK11-4; Sequence=VSP 005659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 reticulon domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Namea is
Name=1: Synonyms=Nogo-A, NI-220-250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Binds to RTN4R. Interacts with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Potent neurite outgrowth inhibitor which may also block the regeneration of the nervous central system in adul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mainly in the nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane of the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ime=3; Synonyms=Nogo-C, VP20;
IsoId=Q9JK11-3; Sequence=VSP_005656,
                                                                                                                                                                                                                                                                                                                                PS50845;
                                                                                                                                                                                                                                                                                                                                                                  IPR003388; Reticulon.
                                                                                                                                                                                                  990
1011
1105
1126
976
                                   173
   192
                                                                                                                                                                                                                   989
1010
1104
1125
1163
                                                                                                                                                                                                                                                                                                                                RETICULON; 1.
                                 975
   975
                                                                                          975
                                                                                                                                                                                                                                                                                         Alternative splicing; Transme CYTOPLASMIC (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (By similarity).
             /FTId=VSP_005657.
Missing (in isoform
/FTId=VSP_005658.
                                                                                    /FTId=VSP_005656
AVLSAELSKTS -> MI
Missing
                                                                                                           Missing (in isoform 3).
/FTId=VSP_005656.
                                                                                                                                                                                 POLY-GLU
                                                                                                                                                                                                    RETICULON.
                                                                                                                                                                                                                   POTENTIAL.
CYTOPLASMIC (Potential).
                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                         LUMENAL
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   (In isoform 4)
                                                                                                                                                                                                                                                         (Potential)
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                                                                                          MDGQKKHWKDK
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RESULT RTN4_RA

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RESULT 48

OSH1 YEAST

ID OSH1 YEAST STANDARD; PRT; 1188

AC P35845; P39555; P80234;

DT 01-UUN-1994 (Rel. 29, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence upda

DT 28-FEB-2003 (Rel. 41, Last annotation up

DE Oxysterol-binding protein homologic
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Best Local S
Matches 170
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SEQUENCE
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                                                                                                                                                                                                                                                           AEAEKLLALLKGSNPSSVSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDA-----DVKANPTGDSAA-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAPRDQEFYDKAYNLLTEAHKALFXNKG--RNSDFQALDKLLERLNDESTNKEKLVDDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSH-TLTAKKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDSEAD-----YVTTDTL----SKVTEAAVSN--MPEGLTPDLVQEACESE
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                                                                                                                                                                                                                                                                                                        SFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTFPLLEDHTSENKTDEKKIEERKAQIITEKTS--PKTSNPFLV-----AV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAPVREEYADFKPFEQAWEVKDTYEGSRDVLAARA-NVESK--VDRKCLEDSLEQK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQIVIKITD-QGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGY
                                                                                                                                                                                                                                                                                                                                                  EVPQV---
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Pred. No. 10;
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MISSING (IN REF. 3; /
WW; 8CB894B09E94F0B6
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Hall J., Ou
Storms R.K.
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                    Pfam; PF01237; Oxysterol_BP; Pfam; PF00169; PH; 1. SMART; SM00248; ANK; 2.
                                                                                              SGD; S0000082; OSH1.
GO; GO:0005769; C:early endosome; IDA.
GO; GO:0000138; C:Golgi trans cisterna;
GO; GO:0000138; C:Golgi trans cisterna;
GO; GO:0005545; F:phosphatidylinositol b
InterPro; IPR002110; ANK.
InterPro; IPR001648; Oxysterol_BP.
InterPro; IPR001649; PH.
                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                         EMBL; L28920; AAC09497.1;
EMBL; L28920; AAC09496.1;
EMBL; X74552; CAA52646.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics 157:1117-1140(2001).
-!- FUNCTION: PLAYS A ROLE IN ERGOSTEROL
-!- SUBCELLULAR LOCATION: Found in Golgi
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MEDLINE=21135676; PubMed=11238399;

Beh C.T., Cool L., Phillips J., Rine J.;

Beverlapping functions of the yeast oxysterol-binding homologues.";
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MEDLINE=21301806; PubMed=11408574;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                     InterPro; IPR001849
Pfam; PF00023; ank;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Levine T.P., Munro S.;
"Dual targeting of Oshlp, a yeast homologue of oxysprotein, to both the Golgi and the nucleus-vacuole Mol. Biol. Cell 12:1633-1644(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jiang B., Brown J.L., Sheraton J., Fortin N., Bussey H.; "A new family of yeast genes implicated in ergosterol synthesis "Related to the human oxysterol binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94287711;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 1 PH domain.
SIMILARITY: Contains 3 ANK repeats.
CAUTION: Ref. 1 sequence differs fro
frameshift in position 230.
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SIMILARITY: BELONGS TO
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., Kaback D.B., Zhong W., Vo
Quellette B.F.F., Keng T.,
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AAC09496.1; ALT_FRAME.
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3; Mismatches 256;
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UN89_CAEEL
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001761; Q17362;
15-SEP-2003 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Structural component of the muscle M-line. Myofilament lattice assembly begins with positional cues laid down in the basement membrane and muscle cell membrane. UNC-89 responds to these signals, localizes, and then participates in assembling an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Muscle M-line assembly protein unc-89 (Uncoordinated UNC-89 OR CO9D1.1.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    these signals, localizes, and then participates in a W-line.

TISSUE SPECIFICITY: Localizes to the middle of A-ban-
SIMILARITY: Contains 1 DBL-homology (DH) domain.

SIMILARITY: Contains 1 fibronectin type III domain.

SIMILARITY: Contains 49 immunoglobulin-like C2-type.

SIMILARITY: Contains 1 PH domain.

SIMILARITY: Contains 5 RCSD domains.

SIMILARITY: Contains 5 RCSD domains.
                                                                     Pfam;
                                                                                                                    Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                             PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Bristol N2;
Du Z., Le T.T., Wilson R.;
Submitted (MAY-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Benian G.M., Tinley T.L., Tang X., Borodovsky M., "The Caenorhabditis elegans gene unc-89, required assembly, encodes a giant modular protein composetransduction domains.";
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MEDLINE=96180278; PubMed=8603916;
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Rhabditidae; Peloderinae;
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1; PF00169; PH; 1.
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17; SM0040B; IGC2; 23.
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PROSITE; PS50010; DH 2; 1.

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PROSITE; PS50003; PH_DOWAIN;

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  Immunoglobulin domain; Repeat; SH3 domain;
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                          KKDK-SPEKSITEEIKSPVKKEKS----PEKVEEKPASPTKKEKSPEKPASPTKKSEN
                                                                           ADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEH----TVEVKNGNL-IIPHKDHYH
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                                                                                                    MEDLINE=96196435; PubMed=8648631;
Baumgartner R., Czisch M., Mayer U.,
Timpl R., Holak T.A.;
"Structure of the nidogen binding LE
chain in solution.";
J. Mol. Biol. 257:658-668(1996).
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                                                                                                                                                                                                                            factor-like (LE) modules of laminin
nidogen binding site.";
J. Mol. Biol. 257:644-657(1996).
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Ogawa K., Burbelo P.D., Sasaki M., Yamada Y.;
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Sasaki M., Yamada Y.;
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Mammalia; Eutheria; Rodentia;
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LAMC1 OR LAMC-1 OR LAMB-2.
Mus musculus (Mouse).
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01-JUL-1989 (Rel. 11, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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Biol. (
SUBUNIT: Laminin is a complex glycoprotein, different polypeptide chains (alpha, beta, to each other by disulfide bonds into a cro
                                        FUNCTION: Binding to cells via a high affinity receis thought to mediate the attachment, migration, are of cells into tissues during embryonic development with other extracellular matrix components.
                                                                                         function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      laminin B2 chain promoter contains unique repeat sequences and ctive in transient transfection."; iol. Chem. 263:8384-8389(1988).
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os B.B., Liu S.-H.,
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                 consisting of three
gamma), which are bo
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SMART; SM00281; LamB; 1.

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PROSITE; PS00022; EGF 1; 8.

PROSITE; PS01186; EGF 2; 2.

PROSITE; PS01248; LAMININ_TYPE_EGF; 10.
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GO; GO:0005604; C:basement membrane;
InterPro; IPRO66209; EGF like.
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Pfam; PF00053; laminin_EGF; 10.
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SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: FOUND IN THE RACEVILLAR COMPONENT).
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DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
SIMILARITY: Contains 1 laminin N-terminal domain.
SIMILARITY: Contains 11 laminin EGF-like domains.
SIMILARITY: Contains 1 laminin IV domain.
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1KLO; 20-AUG-97.
1TLE; 12-FEB-97.
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; Laminin_EGF.
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1243 DLEKQAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIK	ф
563 DKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVK	Ş
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O1-JUN-2003 (TremBirel. 23, Last annotation updat

Tremmococcal histidine triad A protein.
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Choi G.H., Barash S.C., Rosen C.A., Masure H.,
Gayle A., Brewah Y.A., Walsh W., Barren P., L.
Langermann S., Johnson S., Koenig S.;
"Use of a Whole Genome Approach To Identify V.
Affording Protection against Streptococcus pn
                                                                                                                                 Infect. Immun. 69:1593-1598(2001).
EMBL; AF291695; AAK19155.1.
InterPro; IPR006270; Strep_his_triad.
TIGRRAMs; TIGR01363; strep_his_triad; 2.
SEQUENCE 816 AA; 91519 MW; 5359126A611D27ED CRC64;
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Bacteria; Firmicutes; Lac
Streptococcus.
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H.R., Tuomanen E.,
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ID Q8DPQ2;
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AC Q8DPQ2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence updat DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation upc Pneumococcal histidine triad protein A.
GN PHTA OR SPR1061.
GN Streptococcus pneumoniae (strain ATCC BAA-255 / OS Streptococcus pneumoniae)
OC Bacteria; Firmicutes; Lactobacillales; Streptoc OC NCBI TaxID=171101;
RP SEQUENCE FROM N.A.
RX MEDLINE=21499245; PubMed=11544234;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcz
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D. Bacteriol. 183:5709-5717(2001).

REMBL, AE008479; AAK99865.1; -.

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   LLKGSNPSSVSKEKIN
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ilarity 99.7%;
Conservative
                          796
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Pred. No. 2.8e-229;
0; Mismatches 2;
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Best Local
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Q9AG74;
Q1-JUN-2001
01-JUN-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from Streptococcus pneumoniae, Processor from Streptococcus pneumoniae, Processor from Streptococcus pneumoniae, Processor from Streptococcus para (2001).

Infect. Immun. 69:3827-3836 (2001).

EMBL; AR340221; ARX26629 1; -

InterPro; IPR006270; Strep_his_triad.

TICRFAMS; TICR01363; Strep_his_triad; 2.

TICRFAMS; TICR01363; Strep_his_triad; 2.

SEQUENCE 844 AA; 94769 MW; D738A55290FF8902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
NEDLINE=21246685; PubMed=11349048;
Zhang Y., Masi A.W., Barniak V., Mountzouros
Green B.A.;
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NCBI_TaxID=1313;
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Bacteria; Firmicutes; Lactobacillales;
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ITSDEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGA
                     IISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSA
                                                              ESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHD
                                                                                                 KQESLSHKLGAKKTDLPSSDREFYNKAYDLLARIHQDLLDNKGRQVDFEALDNLLERLKD
                                                                                                                        KQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLND
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75.3%;
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Last annotation update)
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Pred. No. 1.
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Q8CWR4;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete SEQUENCE
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NCBI_TaxID=171101;
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01-MAR-2003 (TrEMBLrel 23, Last sequence up
01-MAR-2003 (TrEMBLrel 23, Last annotation
Histidine motif-containing protein.
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EMBL; AE008479; AAK99864.1; -.
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"Genome of the bacterium Streptococcus
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MEDLINE=21429245; PubMed=11544234;
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Local Similarity 75.0%;
les 617; Conservative 69
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855 AA;
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                                                         VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGL1FDPAQITSRT
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micutes; Lactobacillales; Streptococcaceae;
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Pred. No. 7.4e-176;
59; Mismatches 99;
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Best Local Similarity
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Q97QM9;
01-OCT-2001
                                                                                                                                                                            MEDLINE=21357209; PubMed=11463916;
Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Angiololi S., Dickinson T., Hickey Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
"Complete genome sequence of a virulent isolate of Streptococcus.
                                                  Complete
SEQUENCE
                                                                                                                                                              "Complete genome pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
STRAIN=TIGR4;
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Streptococcus.
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01-MAR-2003
                                                                                                                 Science 293:498-506(2001).
EMBL; AE007418; AAK75283.1; -.
TIGR; SP1174; -.
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1313;
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                                                                                 InterPro; IPR006270;
TIGRFAMs; TIGR01363;
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                           TETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGS
                                                                                                                                       DLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKPEEET
                                                                                                                                                            DLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEE------
                                                                                                                                                                                                        SPOPAPSNPID--EKLVKEAVRKVGDGYVFEENGVSRYIPAKDLSAETAAGIDSKLAKQE
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KETLTGLKNNLLFGTQDNNTIMAEAEKLLALLKES
                                                                      PREEKPQSEKPESPKPTEEPEESPEESEEPQVETEKVEEKLREAEDLLGKIQDPIIKSNA
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O1-JUN-2001 (TrEMBLrel. 17, Created)

O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)

O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Pneumococcal histidine triad protein B precursor (Fragment)

PHTB.

Streptococcus pneumoniae.

Bacteria; Firmicutes; Lactobacillales; Streptococcaee;

Streptococcus.

NCBI_TaxID=1313;

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Query Match
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Dormitzer M., Dagan R., Brewah Y.A., Barren P., Lathigra R.,
Langermann S., Koenig S., Johnson S.;
"Identification and characterization of a novel family of pneumococcal
proteins (the Pht family) that are protective against sepsis.";
Infect. Immun. 69:949-958 (2001).
EMBL; AF318954; AAK06759.1; -
InterPro; IPR006270; Strep_his_triad.
TIGRFAMs; TIGR01363; strep_his_triad; 2.
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                                                                                                                                                                                                   YNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAMFDDHTYKAPNGYTLE
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TETLAGLRNNLTLQIMDNNS IMAEAEKLLALLKGS
                                    PREEKPQSEKPESPKPTEEPEESPEESEEPQVETEKVEEKLREAEDLLGKIQDPIIKSNA
                                                                                                          DLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKPEEET
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Pred. No. 6.8e-151;
4; Mismatches 140;
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Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Peterson S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Radune D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey I
Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
"Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-21101045; PubMed=11159990;

Adamou J.E., Heinrichs J.H., Erwin A.L., Walsh W., Gayle T.

Dormitzer M., Dagan R., Brewah Y.A., Barren P., Lathigra F.

Langermann S., Koenig S., Johnson S.;

"Identification and characterization of a novel family of proteins (the Pht family) that are protective against seps infect. Immun. 69:949-958 (2001).
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01-JUN-2001 (TrEMBLrel. 17, I
01-MAR-2003 (TrEMBLrel. 23, I
Pneumococcal histidine triad
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TIGRFAMs; TIGR01363; strep_his_triad; 2
Signal; Hypothetical protein; Complete
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POTENTIAL.
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EMBL; AF318955; AAK06760.1;
EMBL; AE007403; AAK75120.1;
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SVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSR
                                                                               TGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVP
                                                                                                                                                                                          AAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIED
                                                                                                                                                           AAHADNIRTKEEIKRQKQEHSHNHGGGS--NDQAVVAARAQGRYTTDDGYIFNASDIIED
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Pred. No. 4.7e-150;
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Q8DQ08;
01-MAR-2003
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                                                                                     Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S. DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.
                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=21429245; PubMed=11544234;

MEDLINE-21429245; PubMed=11544234;

MEDLINE-21429245; PubMed=11544234;
                                                                                                                                                                                                                  Streptococcus.
                                                                                                                                                                                                                          Streptococcus pneumoniae
Bacteria; Firmicutes; Lac
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Pneumococcal histidine triad protein D.
                                                                      Genome of the
  Local
                                                            Bacteriol.
         Match
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                                                 me of the bacterium Streptococcus cteriol. 183:5709-5717(2001). AE008464; AAK99711.1; -.
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Lactobacillales; Streptococcaceae;
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(TrEMBLrel. 17, (TrEMBLrel. 17, )
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l histidine triad
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 293:498-506(2001).
EMBL; AF318956; AAK06761.1;
EMBL; AE007403; AAK75121.1;
TIGR; SP1004; -
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Adamou J.E., Heinrichs J.H., Erwin A.L., Walsh W., Gayle T.,
Dormitzer M., Dagan R., Brewah Y., Barren P., Lathigra R.,
Langermann S., Koenig S., Johnson S.;
"Identification and characterization of a novel family of pneumococcal
proteins (the Pht family) char are protective against sepsis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus.
NCBI_TaxID=171101;
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                            GNAYIVPHGGHYHYIPKSDLSASELAAAKAHLAGKNMQPSQLSYSSTASDN------
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STRAIN-SF370 / ATCC 700294 / Serotype M1;

MEDLINE-21192684; PubMed=11296296;

MEDLINE-21192684; PubMed=11296296;

MEDLINE-21192684; PubMed=11296296;

Perretti J.J. McShan W.M., Ajdic D.J., Savic D.J., Savic G.

Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S.,

Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., Whi

Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

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TIGRFAMS; TIGR01363; strep_his triad; 4.
Hypothetical protein; Complete proteome.
SEQUENCE 825 AA; 92649 MW; 57DF50969)
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01-MAR-2003
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence
01-MAR-2003 (TrEMBLrel. 23, Last annotati
Hypothetical protein spyM18_2072.
Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcus.
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EMBL; AE010110; AAL98543.1; -
InterPro; IPR006270; Serp_his_triad.
TIGRRAMS; TIGR01363; strep_his_triad; 4.
Eypothetical protein; Complete proteome.
SEQUENCE 823 AA; 92585 MW; C79E1EB30CEEDF0C (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Smith T.M., Zhang Q.,
Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microarray analysis of serotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cutbreaks.";
Froc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       group A Streptococcus strains associated with acute rheumatic fever
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                                   SFVIPHIDHIHVVPYSWL---
                                                                               TQIAFAEQELMLKDKKHYRYDIVDTG-----IEPRLAVDVSSLPMHAGNATYDTGS
                                                                                                     AAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNG
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Pred. No. 8
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                                   -TRDQIATIKYVMQHPEVRP---DVWSKPGH
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SEQUENCE FROM N.A.
STRAIN-NEM316 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C.,
Glaser P., Zouine M., Couve E., Laliou
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01-MAR-2003 (TrEMBLrel.
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SEQUENCE 822 AA; 92393 MW; 2929A97C8AFCD78F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of Streptococcus and invastive neonateal disease.";
Mol. Microbiol. 45:1499-1513(2002).
EMBL; AL766850; CAD46965.1; -.
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                    KGIS-RYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEA 450
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                                                               AGQTEDN----DSGSEHSKPSDK---
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Pred. No. 1e-45;
Mismatches 265;
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TIGRFAMS; TIGR01363; Strep_his_triad; 4.
SEQUENCE 825 AA; 92623 MW; DE4ECC199181DFFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           Terao Y., Kawabata S., Hamada S.; Characterization of a novel histidine triad p streptococci."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ EMBL; AB073859; BAB71774.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
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     IFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLS---GRGNLSNSRTYRR
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                                          KPGSKRKNIRTKQQIAEQVAKGTKEAKEKGLAQVAHLSKEEVAAVNEAKRQGRYTTDDGY
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01-OCT-2002
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STRAIN-MGAS315 / Serotype M3;
MEDLINE=22133808; PubMed=1212206;
Beres S.B., Sylva G.L., Barbian K.D., L.
Mammarella N.D., Liu M.-Y., Smoot J.C.,
Campbell D.S., Smith T.M., McCormick J.
Schlievert P.M., Musser J.M.;
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01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Histidine triad protein
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                               NCBI_TaxID=198466;
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Lactobacillales;
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C., Porcella S.F.
J.K., Leung D.Y.!
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EMBL; AE014169; AAM80331.1; -
InterPro; IPR006270; Strep_his_triad.
TIGRPAMS; TIGR01363; strep_his_triad;
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823 AA; 92431 MW; 8C6CBD517A2DD616
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                                                                    WKDGSFSIPRADGSSLRTINKSDLSQAEWQQAQELLAKKN----AGDATDT--
                                                                                                                                             EESGSVI PNVTPLDKRAGMPNWQI IHSAEEVQKALAEGRFATPDGYI FDPRDVLAKETFV
                                                                                                                                                                                                                      SFVIPHIDHIHVVPYSWL-
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                                LQIMDNNSIMAEAEKLLALLKGSNPSSVSKEK 794
                                                                                                           ----VPQVE-----TEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLT
                                                                                                                                                                               GNASEHVLGKKDHSEDPNKNFKADEEPVEETPAE----PE----
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DKPKEKQQADK---SNENQQPSEASKEE
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SEQUENCE FROM N.A.

STRAIN=2603 V/R / Serotype V;

MEDLINE=2222988; PubMed=12200547;

Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.

Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.

Messels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,

Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,

DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,

Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,

Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,

Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora

lacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione

Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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ALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTE
                                                                                                                          GISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHK
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Pred. No. 2.9e-45;
                                                              SKPSDKE-VTHTFLGHR-----IKAY-----
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Q9ZHG7;
Q9ZHG7;
01-MAY-1999
01-MAY-1999
01-MAR-2003
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                                                                                                                                                                                                                                                                                                   Hypothetical protein. SEQUENCE 822 AA; 9
                                                                                                                                                                                                                                                                                                                                    InterPro; IPR006270; Strep_his_triad.
TIGRFAMs; TIGR01363; strep_his_triad;
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  KDAAHADNVRTKEEINRQKQEHSQH-REGG-----TPRNDGAVALARSQGRYTTDDGY
                                                                                         YVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYL
                                                                                                                                        SYQLGKHHMGLATKDNQIAYIDDSKGKVKAPKT-NKTMDQISAEEGISAEQIVVKITDQG
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                                                               YVTSHGDHYHFYNGKVPYDAIISEELLMTDPNYHFKQSDVINEILDGYVIKVNGNYYVYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                 92386 MW;
                                                                                                                                                                                                                   Score 934; DB 2;
Pred. No. 4.2e-45;
9; Mismatches 235
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SEQUENCE PROM N.A.
STRAIN=NEM316 / Serotype III;
STRAIN=NEM316 / PubMed=12354221;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser
                                                                                                                                      Streptococcus agalactiae (serotype III Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                                                               Hypothetical GBS1925.
                                                                                               NCBI_TaxID=216495;
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                                                         WEDLINE=21172873; PubMed=11274116; Granlund M., Michel F., Norgren M.; Withually exclusive distribution of IS1548 II intron identified in human isolates of g J. Bacteriol. 183:2560-2569 (2001). EMBL; AU29052; CR035985.1; InterPro; IPR006270; Strep_his_triad. INGRPAMS; TIGR01363; strep_his_triad; 1.
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Q9AE21;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Hypothetical 32.0 kDa protein (Fragment).
Streptococcus agalactiae.
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Hypothetical protein SEQUENCE 481 AA;
Hypothetical protein.
NON TER 289 28
SEQUENCE 289 AA; 3
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                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Mol. Microbiol. 45:1499-1513(2002)
EMBL; AL766854; CAD47584.1; -.
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Q8E5R2;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=NEM316 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C.,
                                                                                                                                                                                                                  Hypothetical SEQUENCE 8
                                                                                                                                                                                                                                     SagaList; gbs0918;
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                                                                                                        QGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYV 115
                                                                                                                                                  KENNRVSYIDGKQATQKTENLTPDEV----SKREGI---
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            QEHKNSHHIKTKQVAKKKANKKKVSVKESHKKRKGVAGVDFPTDDGFLLTKDSKILSHPD
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IVSEDANGYVVRHGDHFHYIPKASLSQQKQVQASRAVSRLGNQNNS--HYRVNSSKIA--
                                         YLIPNANA-KTNKKQAVRNFKA-
                                                             YLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASD 175
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Last annotation updat
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Pred. No. 3.9e-09;
5; Mismatches 272;
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Pred. No. 3.3e-31;
0; Mismatches 61;
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Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Macoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C. DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mor
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                                                               HNNISDLTPLSNLTKLQELYLDHNNVKNLSA-LSGKKDLKVLDLSNNKSADLSTLKTTSL
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                                                                                                                                              FLDKMPLLEGLDISQNG--IKDLSFLTKYKQLSLIAAANNGITSLKPLAELPNLQFLVLS
                                                                                                                                                                                      Y--KAP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KENNRVSYIDGKQATQKTENLTPDEV----SKREGI------NAEQIVIKITD
                                                                                                                                                                                                                            TKINIGQRTNPFQRFGLSLMPNIEVL-GIGFTPINDMTPVLQFKKLKQLWMTNTGITDYS
                                                                                                                                                                                                                                                                  YNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKD-----HYHNIKFAW-----FDDHT
                                                                                                                                                                                                                                                                                                           I PDGHHDHSHAKDKV-GMATLKQIGFDDEII QDILHADAPTPFPSNETNPEKMRQWLATV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHDDHTHVIMAKDI ---
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877 AA; 97563 MW;
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                                                                                                                                                                                      NGYTLEDLFATIKY
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  PEVPQV-
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Pred. No. 5.
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                                                                                                     DGWGNASEHVLGKKDHSE-
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Best Local
                                                                                                             299276 PRELIMINARY; PRT; /yz Am.
299276; O1-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Putative internalin A precursor.
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Q8DQ06;
01-MAR-2003
                    NCBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TTEMBLrel 23, C
01-MAR-2003 (TTEMBLEL 23, I
01-MAR-2003 (TTEMBLEL 23, I
Fneumococcal histidine triad
FHTE-TRUNCATION OR SPR0910.
                                    Streptococcus
                                                             Bacteria; Firmicutes; Lactobacillales;
                                                                                  Streptococcus pyogenes.
                                                                                                      INLA OR SPY1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae (strain ATCC BAA-255 / R6). Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21429245; PubMed=11544234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome of the bacterium Streptococcus 7. Bacteriol. 183:5709-5717(2001).
                                                                                                                                                                                                                                                                                  24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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31.6%;
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Last annotation update)
Id protein E, truncation.
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Pred. No. 1.5e-06;
6; Mismatches 50;
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                                                           Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae strain R6.";
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D.-J., Fuller W., Geringo
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Geringer C.,
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Matches 168
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MEDLINE=21192684; PubMed=11296296;

Perretti J.J., McShan w.M., Ajdic D.J., Savic G., Lyon K., primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McQ., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe G.A., McQ., Sin Y., Streptococcus pyogenes.";

"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";

Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
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InterPro; IPR001611; LRR.
InterPro; IPR007092; LRR SDS22.
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STRAIN=SF370 / ATC
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                  LTNVNLSKPNKTVTNIDISH--NNISLADLKLNEQHIPEAIAKN---FPAVYEGSMVGNG
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                                                             YVTPHMGH-----
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19.5%;
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                                                           -SHWIGKDSLSD---KEKVAAQAYTKEKGILPPSPDADVKANP
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Pred. No. 0.00016;
l6; Mismatches 279;
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STRAIN-MGASJ15 / Serotype M3;

MEDLINE=22133808; PubMed=12122206;

Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,

Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins :

Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,

Schlievert P.M., Musser J.M.;

"Genome sequence of a serotype M3 strain of group A Streptococc phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE014157; AAM79642.1; -.
InterPro; IPR007092; LRR SDS22.
PROSITE; PS50504; LRR SDS22; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 792 AA; 87476 MW; 1D501C439CAE224B
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INLA OR SPYM3_1035.
Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales;
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01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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01-OCT-2002
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Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
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 PSPGPQP---APNLKIDSNS--
                               --IGKDIP----DPHAIEHARELEKHKFGMDTLRALGFDEEVILDIVRTHDAPTPFPSNE
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Last sequence update)
Last annotation updat
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Pred. No. 0.0006;
1; Mismatches 211;
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Eukaryota; Alveolata;
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Theisen M., Thomas A.W., Jepsen S.;
"Cloning, nucleotide sequencing and analysis of the glutamate-rich protein (GLURP) from Plasmodium reich
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 KVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYD
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                                                                                        LNE-
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                                                                                                                                                                                                                                       QGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYH----YIPKNELSASELAAAEAFLSGR
                                                                                                                                                                                                                                                                                                 VYLKDAAH--ADNVRT-----KEBI----NRQKQEHSQ---HREGGTPRNDGAVALARS 159
                                                                                                                                                                                                                                                                                                                                                                                        HNVNVLQENNINNHQLEPQEKANIESFEPKNIDSEIILPENVEKEEIVVDVPSPKHFNHE
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                             VSE-RSASE---PSEHVESVSEQSNNEPSEKKDGPVPSKPFEEIEKVDVQPKIVDLQIIE
                                                         IIPLRYRSNHWVPDSRPEQPSPQPTPEPS---PGPQPAPNL----KIDSNSSLVS-QLVR
                                                                                                                 LKQLYKLPLSQRHVESDGLVFDPAQ-ITSRTARGVAVPHGDHYHFIPYSQMSELEERIAR
                                                                                                                                                                              GNLSNSRTYRRQNSDNT----SRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSL
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077033;
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J. Biol. Chem. 0:0-0(1998).
EMBL; AB009980; BAA33143.1; -.
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TRFA.
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Pfam; PF00515; TPR; 9.
SMART; SM00028; TPR; 9.
SEQUENCE 1390 AA; 1604;
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NCBI_TaxID=44689;
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Pred. No. 0.02;
1; Mismatches 291;
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proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002)
EMBL; AE010057; AAL97968.1; -.
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MEDLINE=21927593; PubMed=11917108;

Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,

Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,

Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,

Kapur V., Daly J.A., Veasy L.G., Musser J.M.;

"Genome sequence and comparative microarray analysis of serotype M18
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01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Streptococcus pyogenes
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01-OCT-2002
PFAM; PF00560; LRR; 4.
PROSITE; PS50504; LRR SDS22; 1.
COmplete proteome; Hypothetical SEQUENCE 792 AA; 87440 MW; 5
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InterPro; IPR007092; LRR_SDS22.
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                                                                    PRELIMINARY;
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Matches 150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
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                                                                                                             NHFLHNNNNDSYNYDIYNHFHTYNNCNLYNDDKNELS-----KKG-
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                                                 ----AVLNRYNEQEQNIPIEHEYNNISYPSLIKNN---KNNS----EKKYLDNLSINL
                                                                              TGDSAAAIYNRV-KGEKRIPL-----VRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAW
                                                                                                                                             EHDIISDEGDAYVTPHMGHSHWIGKDSL--SDKEKVAAQAYTKEKGILPPSPDADVKANP
                                                                                                                                                                                                          NDESTN-KEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFD
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17.6%; Pred. No. 0.22;
ative 134; Mismatches
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C15754; O15700;
O1-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-OCT-2002 (TrEMBLrel. 2
QEIJ56;
QEIJ56;
QEIJ56;
01-MAR-2003 (Tr)
01-MAR-2003 (Tr)
01-MAR-2003 (Tr)
Glutamate-rich J
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Submitted (AUG-1997) to the EMBL/GenBank/DDBJ
EMBL; AP020407; AAC16025.1; -
NON_TER 565
SEQUENCE 565 AA; 62729 NW; B059B6E08201E1C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dictyostelium discoideum (Slime mold). Eukaryota; Mycetozoa; Dictyosteliida; NCBI_TaxID=44689;
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Last
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Pred. No. 0.03
60; Mismatches
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Plasmodium falciparum |
Eukaryota; Alveolata; F
NCBI TaxID=36329;
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EMBL; AE014834; AAN35541
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                                            EPDQNDSELSENELVESEKSVSEPAEHVEIVSEKSVSEPAEHVEIVSEKSTSEPAEHVES
                                                                                                 EHEEVVSEESNPEPAENEESSIEEAHQEEIVPEQNDEESGESGLVDNEEGDFEEPNHEEF
                                                                                                                                                      HHEETVPEONNEESGESKLVDNDEGGFEEAHHENFSSEVSNSELNENEFVESDKSVTEPA
                                                                                                                                                                                 VSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNS-----DFQALDK-----
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                                                                -PERLGKPNSQIEYTEDEVRIAQLADKY-TTSDGYIFD--EH-DIISDEGDAYVTPHMGH
                                                                                                                                                                                                            PEKADN---DGNVSQNSN------NELNENEFVESEKSEHEPAENEESSL--EEG
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Apicomplexa; Haemosporida;
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Pred. No. 0.11;
41; Mismatches 3
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    EKVAAQAYTKEKGILPPSPDADVKANPTG--DSAA
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SEQUENCE
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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01-NOV-1996 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
Glutamate rich protein.
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Borre M.B., Dziegiel M., Hogh B., Petersen E., Rieneck K., Riley E Meis J.F., Aikawa M., Nakamura K., Harada M., Wind A., Jakobsen P.I. Cowland J., Jepsen S., Axelsen N.H., Vuust J.:
"Primary structure and localization of a conserved immunogenic "Primary structure and localization of a conserved immunogenic Plasmodium falciparum glutuamate rich protein (GLURP) expressed in lette preerythrocytic and erythrocytic stages of the vertebrate life
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Eukaryota; Alveolata; Apicomplexa; Haemosporida;
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                              SEQUENCE
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EMBL; M59706; AAAS0613.1; -.
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                                                                                                                                                                                                                                                              1271 AA;
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                                                                                                                                                                                             4.2%; Score 176.5; D
19.1%; Pred. No. 0.14;
                                                                                                                                                                                                                                                              145476 MW;
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OPGTX2
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Glutamate-rich protein.
GLURP
SEQUENCE FROM N.A.

STRALM=FCC1/HN;

STRALM=FCC1, Yu X.B., Li X.R., Ma C.L., Fang J.M.;

Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M.;

"Molecular cloning and structure of the glutamate rich p

gene of Plasmodium falciparum isolate FCC1/HN.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                      Eukaryota; Alveo
NCBI_TaxID=5833;
                                                                                                                                          ıkaryota; Alveolata;
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InterPro; IPRO05479; CPBSe L D2
PROSITE; PS00867; CPBASE 2; 1.
SEQUENCE 1236.AA; 141482 MW;
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nilarity 17.8%;
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Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K. Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angluoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.,
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NCBI_TaxID=36329;
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 DIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDAD--VKANPTG
                                                                                                                              LLTEAHKALFXNK---GRNSDFQALDKLLERLND----------
                                                                                                                                                                                             VFAKDLPSETVKNLESKLSKQESV---SHTLTAKKENV-----APRDQEFYDKAYN
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                                                                                              VSEQAEEEVYINEEILKESSÖVEDVKVENELMNEEVNEETQSVAENNEEDKELDNYVVEE
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Best Local Sin
Matches 182;
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Q8ICV5;
01-MAR-2003
01-MAR-2003
01-MAR-2003
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Hypothetical protein.

SEQUENCE 1063 AA; 123332 MW; 2A2677237A74C755 CRC64.
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NCBI_TaxID=36329;
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                                                                                                             KSDKKFITFNTFDNHSEGSVIFPMEKYRNFTLPSEEKITSYNFLKKHNSTFDSLEKLDML
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LKSKYKSINNKYNNNNNNNNNNNNNNLESENHIADDAMSISYSCPKENIKKN---
                                                     LKQLYKL----
                                                                                                                                                                                                                           NNNNNNNNNNNKSNSNYYISNDFSKNKLLLNKKNDDHTFL----LSNKKIYDTYKER
                                                                                                                                                                                                                                                                                                                                        --NNDNNINIGCNEGK---NNYFLENNNKDGLRRSSLENLKSKSCHNESLEDDGEYNYHN
                                                                                                                                                                                                                                                                                                                                                                                              TPRNDGAVALARSQGRYTTDDGYIFNAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSDNFNNSYITSSANNNVVSKSGSY----KCDAENNNTNMKDLSDINNNNNNNNNNNN---
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18.2%; Pred. No. 0.11
tive 157; Mismatches
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                                                  ----PLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYS
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                                                                                                                                                                                                                                                                       --IPKNELSASELAAAEAFLSGRGNLSNSR---TYRRQ
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Q9U459; Q9GPG4;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Erythrocyte membrane-associated giant protein antigen 332.
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M., Lu J.H., X "Molecular cloning and structure analysis of the Plasmodium rythrocyte membrane-associated giant protein Ag332 (Pf332) Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                              InterPro; IPR006763; Ag332.
InterPro; IPR001313; Pumilio/Puf.
Pfam; PF04671; Ag332; 138.
SEQUENCE 5458 AA; 615269 MW;
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                      GLYQARTVKENNRVS---YIDGKQATQ---KTENLTPDEVSKREGINAEQIVIKITDQGY
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                                                 Conservative
                                                           4.1%;
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                                              Score 172.5; D
Pred. No. 1.9;
62; Mismatches
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RESULT 38
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Q9LCJ9;
01-OCT-2000
                                 Staphylococcus aureus, and Staphylococcus aureus (strain MW2). Bacteria; Firmicutes; Bacillales;
                                                                                                 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23,
                    NCBI_TaxID=1280,
SEQUENCE FROM N.A.
                                                                        FMTB OR TRUNCATED FMTB OR MW2087.
                                                                                     Truncated FmtB.
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Best Local
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EMBL; AP004829; BAB95952.1; -.
InterPro; IPR000890; Acetate kin.
InterPro; IPR005877; Gpos YSTRK.
Pfam; PF04450; YSIRK signal; 1.
TIGRPAMS; TIGR01168; YSIRK signal; 1.
PROSITE; PS01075; ACETATE KINASE 1; 1.
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Baba T. Takeuchi F., Kuroda M., Yuzawa
Nagai Y., Iwama N., Asano K., Naimi T.,
Yamamoto K., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20348625; PubMed=10896508;
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                                                                                                                                 NLLTEAHKALFXNKGRNSDFQALDKLLER-LNDESTN----KEKLVDDLLAFLAPITHP
                                                                                                                                                               TDDNGVDQ---AKDAGKNSIQSTQPATSVKSNAKNDVDQAVTTQNQAI-----
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                               D-VAKDELATKANEQKALTAQTADATT-----EEKEQANQQVDAQLT--QGNQNIENA
                                                                ERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGK
                                                                                                GATTEE-----KNAAKDLVLKAKEKAYQDILNAQTTNDVTQIKDQAVADIQGITADTTIK
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DSUSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMV
                                                                                                                                                                                                                                                                   PDSRPEQPSPQPTPEPSPGPQPA-----PNLKIDSNSSLVSQLVRKVGEG-----YV
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Kuroda H., Cui L.,
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Q9LCH2;
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InterPro; IPR005877; Gpos YSIKK.
InterPro; IPR001899; Gram pos anchor.
Pfam; PF04650; YSIKK signal; 1.
TIGRFAMs; TIGR011168; YSIKK signal; 1.
SEQUENCE 2478 AA; 262995 MW; 1 C118
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1186
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  VT--
                                              RTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSN--NSNTNSQASQSNDIDSLLKQLYKLPL
                                                                                                                                                          RYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNS
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- QANSNIEAANSQNDVDQAKTTGENSIDQVTPTVNKKATARNEITAILNN - -
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19.4%; Pred. No. 0.66;
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FMTB (MRP) OR FMTB OR SAV2160 OR SA1964.
Staphylococcus aureus (strain Mu50 / A)
Staphylococcus aureus (strain N315).
Sacteria; Firmicutes; Bacillales; Staph
                                                                                                                                                                       Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shib. Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; Whole genome sequencing of meticillin-resistant Staphylococcus
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01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
   EMBL; AP003364; BAB58322.1; -.
EMBL; AP003136; BAB43253.1; -.
InterPro; IPR000890; Acetate kin
InterPro; IPR005877; Gpos YSIRK.
                                                                                                                   "Whole genome sequencing of aureus.";
Lancet 357:1225-1240(2001).
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MEDLINE=21311952; PubMed=11418146;
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                           -----NNSIMAEAEKLLALLKGSNPSSVSK
                                                            -VDTELNQAKTNVDQSSTNEYVDNAVKEGKAKINAVKTFSEYKKDALAKIEDAYNAKVNE
                                                                                                                                                                                                                                                                                                                                             THPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSH
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                                                                                                                                                                                                                                                                                                                                                                              KNAAKDLVLKAKEKAYQDILNAQTTNDVTQIKDQAVADIQGITAD
                                                                                          -EVLLAKVTDSSLKANATETLAGLRNNLTLQIMD-----
                                                                                                                         -AGKKELDQ----AAADKKTQIEQTPNASQQEINDAKQE
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Best Local Similarity
Matches 173; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harris B., Lennard N., Clark L., Line A., Barron A., Corton C., Berrinan M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B., Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AL84509, CAD52358.1; -.
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Eukaryota; Alveolata;
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                                                     I-SIDDALEKGKLDKSNLSDNEEKL--DV
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NVPSDENTINDKTKEGSTTLKTAMGYITKFKDFIKNKSENYMTT-----
                        --LADKYTTSD-------GYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSD-
                                                                                                                                                              EHENLSAENVPSDENTINDKTKEGSTTL - - - - KTAMGYITKFKDFIQNKSENYMTTKD-
                                                                                                                                                                                           PSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYV----FEEKGISRYVFAKDL
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                                                                            FQALDKLLER----LNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQ
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Pred. No. 1.
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 Query Match
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Matches 169;
                                             InterPro; IPR005877; Gpos YSIRK.
InterPro; IPR001899; Gram_pos_anchor.
Pfam; PF04650; YSIRK signal; 1.
TIGRFAMs; TIGR01168; YSIRK_signal; 1.
SEQUENCE 2478 AA; 263031 MW; 6898
                                                                                                                      "Mrp-a new auxiliary gene essential for optimal expression methicillin resistance in Staphylococcus aureus."; Microb. Drug Resist. 5:9-18 (1999).
EMBL; Y09927; CAB55329.1; ...
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97302526; PubMed=9158773;
Wu S., de Lencastre H., Sali A., Tomasz A.;
"A phosphoglucomutase-like gene essential for the optimal expression of methicillin resistance in Staphylococcus aureus: molecular cloning
                                                                                                                                                                                                                                                                                     Jolly L., Wu S.W., Van Heijenoort J., Mengin-Lecreulx D., Tomasz A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000
01-MAR-2003
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01-MAY-2000
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                                                                                                                                                                                                                                                             "The femR315 gene from Staphylococcus aureus, the which results in reduced methicillin resistance, e
                                                                                                                                                                                                                                                                                                                             STRAIN=COL;
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                                                                                                                                                                                                    STRAIN=COL
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    phosphoglucosamine mutase."
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                                                                                                                                                                                      WEDLINE=99265121; PubMed=10332717;
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Drug Resist.
              Similarity
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              Score 170;
Pred. No. 0
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Mismatches
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annotation update)
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
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Pfam; PF00611; IQ; 1.
SMART; SM00264; BAG; 1.
SMART; SM00015; IQ; 1.
PROSITE; PS50096; IQ; 1.
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SEQUENCE
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Woffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
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NCBI_TaxID=3702;
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InterPro; IPR000048; IO_region.
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v. Columbia;
  RLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVNEVKGGYVIKVDGKYYVYLKDAAHADNVRTKEEI------NROKQEHSQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A
                                                                                                                                                           STDOHIEEKEIVVNGELVMNLLLKLD---AVEGLHPSIREFRKALATE-LSSIQDKLDSL
                                                                                                                                                                                                                                                ---AKKSFTEEEAARIIQSMYRGYDVRRWEPIKKLKEIA---TVREQMGDVKKRIEALEA
                                                                                                                                                                                                                                                                           IPYSQMSELEERIARIIPLRYRS---NHWVPDSRPEQPSPQPTPEPSPG
                                                                                                                                                                                                                                                                                                                                      GSLNALRTEKGSVES-----NSNLQEESNGEIIKPCEAKENREQP-
                                                                                                                                                                                                                                                                                                                                                                                SNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLQEPRNIPVKLSENHLPKPTEPTKRIAKNEPVKSTKKEQSSSSSEASKLPPVCLRVDPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- YH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGGTP------RIDGAVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KREGINAEQIVIKITDQGYVTSHGDHYHYYNGKV---PYDAIISEELLMKDPNYKLKDED
                                                                      KNSCASAEKEAVKEQVEIKSQP-SDSPVNLEHSQLTEENKMV--
                                                                                                                KQESVSHTLTAKKENVAPRDQEFYDKAYNL----LTEAHKALFXNKGRNSDFQALDKLLE
                                                                                                                                                                                                  --PQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLS--
                                                                                                                                                                                                                                                                                                                                                                                                                             PKERNGGSKSVSHPKRMEKSKETKIAAPLSSKKAESRT--VPEACNVKCEDANAEMKMAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KESSNEGRNLESCPSDLHRNEGQITQAKGK----EGNFECNVLSDAEEKSSVINIPVAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRDDVEASE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1043 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GNLSNSRTYRRQNSDNT-----
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18.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -HYIPKNELSASELAAAEAFLSGR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----QDVKEAQNQKNKEEPGQVPYPIFWIPSYGKRKDVEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassicaceae; Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 168.5; DB 10;
Pred. No. 0.31;
8; Mismatches 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSNEDRKKMONGKTVEYPFDISMIKSL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B5E271A02299177B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SRTNWVPSVSNPGTTNTNTS---NN
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190

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463

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142

306

Query Match 4.0%; Score 168.5; DB 5; Length 1708; Best Local Similarity 17.6%; Pred. No. 0.62; Matches 177; Conservative 142; Mismatches 332; Indels 353; Gaps 39; Matches 177; Conservative 142; Mismatches 332; Indels 353; Gaps 39; Oy 24 KQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISE 81 : : : :	RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P., RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P., RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Kerhornou A., RA Line A., Maddison M., Mclean J., Monson D., Lennard N., RA Line A., Maddison M., Mclean J., Monson P., Moule S., Murphy L., RA Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E., RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M., RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K., RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J., RA Sulston J.E., Craig A., Newbold C., Barrell B.G; "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."; RI Nature 419:527-531(2002). DR EMBL, AL929552; CAD51456.1; SQ SEQUENCE 1708 AA; 201666 MW; 46A3F90A1437CE3B CRC64;	Hall N., Bowman S., Churcher C., Quail M., Barrell B.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. [2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=22255708; PubMed=12368867; MEDLINE=22255708; PubMed=12368867; MHALL N., Pain A., Berriman M., Churcher C., Harris B., Harris D., Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K., Burckee C.O., Burrows C., Cherevach I., Chillingworth C., Chillingworth T., Christodoulou Z., Clark R., Corton C., Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,	Chromosome condensation propred450W. Plasmodium falciparum (isol Eukaryota; Alveolata; Apico NCBI_TaxID=36329; [1] SEQUENCE FROM N.A. Devlin K., Baker S., Davies	SULT 44 Q81413 PRELIMINARY; Q81413; PRELIMINARY; Q81413; PREMBLrel. 2 01-MAR-2003 (TrEMBLrel. 2 01-MAR-2003 (TrEMBLrel. 2	QY 717 PEVPQVETEKVEAQLKEAEVILAKVTDSSLKANATETLAGIRNNLTLQIMDNNSIMAEAE 776	QY 625	713SDTNLEKVLRLSPEEHPMSVLNRTDEKQAESAAETEEGY 533 DEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYT
RESULT 45 Q8IEB6 Q8IEB6 PRELIMINARY; PRT; 2651 AA. AC Q8IEB6; PRELIMINARY; PRT; 2651 AA. DT 01-MAR-2003 (TrEMBLrel. 23, Created) DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)	Db 1350 DQYDKLENQIVLPNGRDNHVNVTRNNHIGQDKSTLYHLHMDKNKKRKLNEN 1400 Qy 647 DHTYKAPNG	488 LLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFD	Qy 402DLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKG 459 Db 1137 LTNLLNDIQSNIEEKQKKQQVDENISKKDLENVDLVYK-IEHLQKELNQYKN 1188 Qy 460 RNSDFQALDKLLERLNDESTINKEKLVDD 487 : : : :	Qy 364 APNLKIDSNSSLVSQLVRKVGEGY	257 TNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHG : : : : : :	Oy	657 82 712 123 768

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harris B., Lennard N., Clark L., Line A., Barron A., Corton Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., I Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AL844599; CAD52344-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=36329;
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VEHPDERPH-SNDGWGNASEHVLGKKDHS-------EDPNKNFKADEEPVEETPAEP-
                                                                                                                                                                                                                                                                                                       EKGISRYVFAKDLPSETVKNL---ESKLSKQESVSHTLTAK---KENVAPRDQEFYDKA-
                                                                       I PLVRLPYMVEHTVEVKNGNLI I PHKDHYHNI KFAWFDDHTYKAPNGYTLEDLFATI KYY
                                                                                                                                 HMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKR
                                                                                                                                                            VEDPNGIGEHQNLKEVHEQ-
                                                                                                                                                                                         ITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDE-----GDAYVTP
                                                                                                                                                                                                                        KOMDGPISNVNIPEELHPVAEGSK-----LEEAKERSMDDA-DKGTITEDITV----
                                                                                                                                                                                                                                                                                                                                          IPSTR--------NVMESGSFVSRNEQIIEEKDDKHITDDTTINPS
                                                                                                                                                                                                                                                                                                                                                                     VPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVS---QLVRKVGEGYVFE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGTEG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --SQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRG
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Alveolata;
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                                            RMDEQISRDNETRQLN----QDHESDSKDEIID--
                                                                                                                                                                                                                                                   YNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAP
                                                                                                                                                                                                                                                                                -GEMPNDSIKSVTITESPLRDVEQMIEPIDGKGNEKNNIIGEPQESTTEIR
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18.7%;
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305661 MW; 2702399D3979AA68
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Pred. No. 1.
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Haemosporida;
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A Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
A Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
A Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
Cronin A., Davies R., Douis P., Dear P., Dearden F., Doggett J.,
A Cronin A., Davies R., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
A Cronin A., Davies R., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
A Cronin A., Goble A., Goodhead I., Gwilliam R., Hamlin N.,
A Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
A Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
A Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
A Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
A Oliver K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
A Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
Barrall B.G.,
                                                                                                                               Matches
                                                                                                                                                            Best Local
                                                                                                                                                                                           Query Match
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01-MAR-2003 (TrEMBLrel. 23, Last
01-MAR-2003 (TrEMBLrel. 23, Last
                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                           Nature 419:527-531(2002).
EMBL; Z98547; CAD49084.1;
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Eukaryota; Alveolata;
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RESULT 47
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                                            O97255 PRELIMINARY; PRT; 1826 AA.
O97255;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence up
O1-OCT-2002 (TrEMBLrel. 22, Last annotation
Hypothetical 216.3 kDa protein.
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Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; F
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                                                                                                                                                                                                                                                                                                   LGKKDHSEDPNKN 702
                                                                                                                                                                                                                                                                                                                                                                                                               LDSYPYEMVEHKNKYTSNMNNQYDNKDSSYLYDDVSSSFNNKKYTKLII--KDNLCNNKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNR-----VKGEKRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSD--------
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                   Haemosporida;
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SEQUENCE FROM N.A.
STRAIN=3D7;
STRAIN=99376085;
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EMBL; AL034558; CAB39021.2;
Hypothetical protein.
SEQUENCE 1826 AA; 216250
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Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
Churcher C.M., Craig A., Davies R.M., Devlin K., Holroyd S., Horns
Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Horns
Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
Mungall K., Murphy L., Oliver K., Quall M.A., Rajandream M.-A.,
Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
"The complete nucleotide sequence of chromosome 3 of Plasmodium
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 EADEKKNKMDNMFYNKERNYLINNQE---
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                                                                                                                                                                                                                                                          NVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDD---
                                                                                                                                                                                                                                                                                                 SSFDQKVDIKRGDENDYIYNNNN
                                                                                                                                                                                                                                                                                                                                    SSLVSQLVRKVGE--GYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKE
                                                                                                                                                                                                                                                                                                                                                                                                         SQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNL----KIDSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLKYTNKEKYSNIDSDIYYREEDYPEYYNDVPSRYNDYYNRVSNRNDKKNELNENSYYYK
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                                                                       KHIDENNMYYKHNELLNEYNTIDDPDNLNNNINRNRNIYMHKNRISNEQNNKFNLNNNEL
                                                                                                                                                YGYNHHIVGGTNTTTYLKNLPKKSYKRREESGEINNESMNLESGEEEYRMMQ-KKKNTTF
                                                                                                                                                                                                                          NLDKNN--IYDDKNNIYDD----
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                                  -KEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNR----VKGEKRIP
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                                                                                                                                                                                   ---LLAFLAPI----THPERLGKPNSQ---IEYTEDEVRIAQLADKYTT-
                                                                                                          -SDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSD-------
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Pfam; PF00047; ig; 50.
Pfam; PF00018; SH3; 1.
SMART; SM00408; IGc2; 15.
SMART; SM00326; SH3; 1.
SMOSITE; PS500835; IG LIKE; 50.
PROSITE; PS50083; IG LIKE; 50.
PROSITE; PS50002; SH3; 1.
Immunoglobulin domain; SH3 domain.
SEQUENCE 16215 AA; 1841509 MW; 2
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InterPro; IPR003961; FN III.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Sly MHC.
InterPro; IPR001452; SH3.
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Drosophila Metazoa; Arthropoda; Hagoda; Insecta; Pterygo
Bukaryota; Metazoa; Arthropoda; Hachlycera; Muscomorpha;
Neoptera; Endopterygota; Diptera; Brachlycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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SLS OR D-TITIN OR CG1915 OR CG18242
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    VPHGDHYHYIPKNELSASELAAAE----AFLSGRGNLSNSRTYRRQNSDN----TSRTNW
                                           RQQLKSVQRVTKQIDKFKIEEVELRHLQAQQAITEEYQTGTAEETVVMIDESSKGSISKV
                                                                                                                              VEQVQRTKEIQRLKSMESVEIMEMTDQIDKLITQQQ------NAKDLIPWKEM
                                                                                                                                                                        ADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIE----
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                                                                                                                                                                                                                                                                                                                                                                                   4.0%; Score 166; Dilarity 19.1%; Pred. No. 21; Conservative 126; Mismatches
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STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., E.
Amanatides P.G., Scherer S.E., Li P.W.,
George R.A., Lewis S.E., Richards S., A
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01-MAR-2001 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                         CG1915 protein.
SLS OR CG1915 OR CG18242 OR
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=7227;
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RA Brandon R.C., Mollown V.K., Yandell M.D., Chen L.X.,
RA Wann K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P. V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Broketein P., Botskev S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Gary N.S., Gelbart M.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Meshrefi A.,
RA Rainzzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rainzzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rainzzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rainzzolo M., Pittman G.S., Pan S., Pollard J., Wang A.H., Wang X.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Globs R.A., Myers E. W., Rubin G.M., Venter J.C.,
Theng G., Zhao Q., Zheng L.,
Theng G., Zhao Q., Zheng L.,
Theng G., Zhao Q., Zheng L.,
RA Cheng X., Jan M., Zhang G., Zhao Q., Zheng L.,
RA Cheng R., Shang R., Wenter J.C., Zhu X., Smith H.O.,
RA Cheng R., Shang R
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Submitted (SEP-2002) to the -!- SIMILARITY: CONTAINS 1 SEMBL; AE003473; AAG22226.2;
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Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
An H., Champe M., Davenport L.B., Dietz S.M.,
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Best Local Similarity
Matches 189; Conserv
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InterPro; IPR00359; FN_III.

InterPro; IPR003599; Ig_-Like.

InterPro; IPR0071110; Ig_-Like.

InterPro; IPR007110; Ig_-Like.

InterPro; IPR003508; Ig_c2.

InterPro; IPR003066; Ig_MHC.

InterPro; IPR003066; Ig_MHC.

InterPro; IPR003066; Ig_MHC.

InterPro; IPR003142; SH3

Pfam; PF00041; fn3; 5.

Pfam; PF00047; ig; 39.

Pfam; PF00018; SH3; 1.

SMART; SM00409; IG; 53.

SMART; SM00408; IGC2; 46.

SMART; SM00326; SH3; 1.

PROSITE; PS50835; IG_LIKE; 50.

PROSITE; PS50802; SH3; 1.
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                 GDAYVTPHMGHSHWIGK----
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                                                   PKPTEPQPQPVLWARGQKKPQKPDEQKQELPKSLEIAV-
                                                                                                                                                                                                                                                                                                                                                                                 QEAFSWRQPREPQKFIQVEDSTLLHLQERHDTQEQQLLQQQPVMWD------
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                                                                                                                    QKAYEEATDELTEEPIPQPQPVMWERGKKKP----QKPQEEVTEIPKTLEIAVDTLEEEV
                                                                                                                                                 QEFYDKAYNLLTE----AHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFL
                                                                                                                                                                                 ETKKTAVRRVIPPREPEQKVEQVTLKPTPRPRPKEAVKAEEIQLKPLRSTRPVPQPVEAE
                                                                                                                                                                                                                  E--KGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAP--------RD
                                                                                                                                                                                                                                                  PQEKTFEEAHDELVEPTPVQQPEPVPVMWERGKKKVAQQETVLSQEVVQTSQVVEQQIVE
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                                                                                                                                                                                                                                                                                                                                                  PHGDHYHFIPYSQMSELEERIARIIPLRYRSNH--WVPDSRPEQPSP------QPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18074 AA;
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19.1%;
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                                                                                                                                                                                                                                                                               EPSPGPQPAP-----NLKIDSNSSLVSQLV---RKVGEGYVFE
                                                                                   RLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 166;
Pred. No.
---DSLSDKEKVA-AQAYTKEKGILPPSPDADVKANPTG
                                                                                                                                                                                                                                                                                                                                                                                                                -LPLSQRH-----VESDGLVFDPAQITSRTARGVAV
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MEDLINE-2225708; PubMed=1236880;
Hall N., Pain A., Berriman M., Churcher C., Harris B., natter Hall N., Pain A., Berriman M., Churcher S., Barron A., Brooks K., Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K., Mungall K., Bowman S., Atkin R., Chillingworth C., Burrows C., Cherevach I., Chillingworth C., Buckee C.O., Burrows C., Cherevach I., Clark L., Clark R., Corton C., Buckee C.O., Burrows C., Christodoulou Z., Clark L., Clark R., Corton C., Hance
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EMBL; AL929355; CAD51726.1; -. SEQUENCE 1373 AA; 159691 MW; C49205917D0695C2
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                 TT--DDGYIF--NASDIIEDTGDAYIVPHG--DHYHYIPKNELSASELAAAEAFLSGRGN
                                                                                                                                   DESIKSTNPVLNFTPYELPLNNKLSSDNYNISSNNIPIYEKNYNYQEDAVVPMSATDEQA
                                                                                                                                                                                                        ADNVRTKEEI - - - -
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STMKDKGKIYKLNVMGPKKWKKEVYNIDQGQNDDTDAIEKRDMEKKK----KKKKSGKKN
                                                                                                                                                                                                                                                                      DLILNNPILMNNVFSLRNTKKKIVIDETL--SFLNPYIEEHLRSGGKSYISKDLRKNEQH
                                                                                                                                                                                                                                                                                                                                                                                                         PDRVKSCLITAIFKLCSRNNIRDHVVAKKIIDK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDEVS-----KREGINAEQIVIKITDQGYVTSHGDHYHYYNGKV------PY 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.0%;
                                                                                                                                                                                                    -----NRQKQEHSQHREGGTP-----RNDGAVALARSQGRY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 %; Score 165.5; DB 5;
%; Pred. No. 0.68;
143; Mismatches 293;
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	KLIFLVKSN 1370	1362	ф
	KLLALLKGS 785	777	Ş
136:	ITTKKKAVFINSTNLNILQTLKKIENNINTNVIEVSKMDSLISCFYNNTKVLIKIKIEDN	1302	뭣
776	VTDSIKANATETLAGLRNNLTLQIMDNNSIMAEAE	741	Ş
1301	VDINVDNSDHLNEITKNKKNKGDQFDMIDLNELPKKIDPTKSSDINIEEEKKLWDK 130	1246	Вb
740	EHV-LGKKDHSEDPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKEAEVLLAK	687	Ş
1245	ILSNKWYFTSKKYDNNNDMGGIRKKSLHNEQVENRDVT-KMKVNEKGNNNNNNDGCTNKL 1249	1187	망
989	IIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNAS	630	γQ
1186	ALFNGLISNNSPLKDPIKSSYVSTISMKKNMS	1155	В
629	QAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNL 629	570	Ş
1154	KEFNRFPSDNYHNKINNKTNVYNWKIKGNINTVANNKKELTEKEKMAA	1107	ф
569	EDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAA	512	Qy
1106	RNNVFINEENENEKRTDNVNVDDYNEQNYERF-DDNKDIHYS	1066	망
511	XNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYT	456	Ş
1065	DDDDEEDEEYEDDEEENEEYVDESDDDEDENHDDDDYHEEEQYN	1016	뭥
455	VFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALF	398	Ş
1019	LHNIVNTQKDRYYDEEDDEDEY 101	986	đđ
397	NHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRY 397	338	Qy
985	KKKKKSVQREEAADFNKGIKNDINQTEEDIK	955	ర్జ
337		278	Qy
954	NKNKKNEKNQNDNNNNNNNNNNNNNNNNNHIDGNQNNSEVINKDKVKK 954	908	8
277	LSNSRTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKL 277	218	δ

Search completed: November 14, 2003, 10:36:53
Job time : 120 secs

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Perfect score:
Sequence:
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Maximum !
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Maximum Match 100%
Listing first 100:
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      Pred. No. is the number of score greater than or equal and is derived by analysis
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-09-536-784-182
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ALIGNMENTS

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RESULT 1
US-08-961-083-56
; Sequence 56, Application US/08961083
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Best Local Simil
Matches 796; C
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAY: (301) 309-8512
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 796 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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STREET: 9410 Key West Avenue
CITY: Rockville
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ZIP: 20850
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                                                           241 VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT 300
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                                                                                                                  181 GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
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301 ARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPG
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Similarity 100.0%; Pred. No. 1.3e-314;
96; Conservative 0; Mismatches 0; Indels 0
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INFORMATION FOR SEQ ID NO: 56: SEQUENCE CHARACTERISTICS: LENGTH: 796 amino aci	твцес	NAME: MICCELIE S. MAIKS REGISTRATION NUMBER: 41,971 REFERENCE/DOCKET NUMBER: PB340P3	FILING DATE: OCT-30-1997 ATTORNEY/AGENT INFORMATION:	PRIOR APPLICATION NUMBER: 08/961,083	FILING DATE: 30-Oct CLASSIFICATION: <ur< td=""><td>CUR</td><td>,</td><td>COMPUTER: HP Vectra 486/33</td><td>COMPUTER READABLE FORM: MEDIUM TYPE: Diskette.</td><td></td><td>STATE: M</td><td>STREET: 9410 Key West Avenue</td><td>CORRESPONDENCE ADDRESS: ADDRESSEE: Human Genome Sciences</td><td>NUMBER OF SEQUENCES: 452</td><td>APPLICANT: Choi et. al.</td><td>GENERAL INFORMATIO</td><td>SOLT 2 -09-53 Sequen</td><td>781</td><td> </td><td>101 TIVONNOCHOMENTAL 100</td><td>. د</td><td></td><td>/ 661 LFATTKYYVEHPDERPHSNOGWGNASEHVLAKKHSEDPNKAFKADEEPVETTPAGEEVP 720</td><td>A O O THE THE THE THE THE THE THE THE THE THE</td><td>601 NRVKOBKRIBUVRLEYMVEHTVEVKNONLITEHKOHYHNIKFAMFDDHTYKARNGVTLED 66</td><td>541 EGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIY 60</td><td>/ 541 EGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIY 600</td><td>481 KEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD 540</td><td>481</td><td>421 VSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTN 480</td><td>421</td><td>361 PQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQES 420</td><td>361</td><td>301 ARGVAVPHGDHYHFIPYSQMSBLBERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPG 360</td></ur<>	CUR	,	COMPUTER: HP Vectra 486/33	COMPUTER READABLE FORM: MEDIUM TYPE: Diskette.		STATE: M	STREET: 9410 Key West Avenue	CORRESPONDENCE ADDRESS: ADDRESSEE: Human Genome Sciences	NUMBER OF SEQUENCES: 452	APPLICANT: Choi et. al.	GENERAL INFORMATIO	SOLT 2 -09-53 Sequen	781		101 TIVONNOCHOMENTAL 100	. د		/ 661 LFATTKYYVEHPDERPHSNOGWGNASEHVLAKKHSEDPNKAFKADEEPVETTPAGEEVP 720	A O O THE THE THE THE THE THE THE THE THE THE	601 NRVKOBKRIBUVRLEYMVEHTVEVKNONLITEHKOHYHNIKFAMFDDHTYKARNGVTLED 66	541 EGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIY 60	/ 541 EGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIY 600	481 KEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD 540	481	421 VSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTN 480	421	361 PQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQES 420	361	301 ARGVAVPHGDHYHFIPYSQMSBLBERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPG 360
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; Patent No. 6582706
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TYPE: amino acid
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STRANDEDNESS: single
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TOPOLOGY: linear
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MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ
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APPLICANT: Johnson, Leslie S.
APPLICANT: Adamou, John E.
TITLE OF INVENTION: Vaccine Compositions
TITLE OF INVENTION: Pneumoniae Group A.
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-444
CURRENT APPLICATION NUMBER: US/09/468,65
CURRENT FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR PILING DATE: 1998-12-21
NUMBER OF SEO ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 819
TYPE: PRT
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
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Similarity 99.9%;
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APPLICANT: Adamou, John B.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structu
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-444
CURRENT APPLICATION NUMBER: US/09/468,656A
CURRENT FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 819
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US-09-468-656A-10
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Best Local Similarity
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ORGANISM: Streptococcus pneumoniae
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                   DEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAI
                                                                             NKEKLVDDLLAFLAPITHÞERLGKÞNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIIS
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DEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYAEEKGLTPPSTDHQDSGNTEAKGAEAI
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US-09-468-656A-4
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CURRENT FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 541;
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TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Stru
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-444
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TYPE: PRT
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; Pred. No. 1.4e-206;
91; Mismatches 144;
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; Patent No. 6159469
; PATENT INFORMATION:
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                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Hr VCC MSDO
OPERATING SYSTEM: MSDO
OPERATING SYSTEM: MSDO
OPERATION DATE
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NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 NAME: Brookes, A. Anders REGISTATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: PB TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
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TOPOLOGY: lin
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9410 Key West Avenue
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                   63.6%;
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                    Score
Pred.
                   2649.5; DB
No. 4e-197;
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US-09-536-784-66
US-09-536-784-66
; Sequence 66, Application
; Patent No. 6573082
; GENERAL INFORMATION;
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COUNTY, 20850
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3
                                                                                                                                                                                APPLICANT: Choi et. al. TITLE OF INVENTION: Streptococcus NUMBER OF SEQUENCES: 452
                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome
STREET: 9410 Key West Av
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      587
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                                                                                 STATE: Maryland COUNTRY: USA
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                    486/33
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                                    1.4Mb
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763 743

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586 595 526 535 466 475 415 346 359 286 299 227

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US-09-536-784-66
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REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 763 amino acids
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nes 519; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <Unknown>
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587
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                               AAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNG
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AEAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKG
                                                                                         DITSDEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKG
                                                                                                                                  DIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDS
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STRANDEDNESS: single
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66.8%; Pred
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US-09-468-656A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Johnson, Leslie S.
APPLICANT: Adamou, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
TITLE OF INVENTION: Motifs
TITLE OF INVENTION: Motifs
TITLE OF INVENTION: Motifs
TITLE OF INVENTION NUMBER: US/09/468,656A
CURRENT APPLICATION NUMBER: US/09/468,656A
CURRENT FILING DATE: 1999-12-02
PRIOR APPLICATION UNMBER: 60/113,048
PRIOR FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
mes 259; Conserv
                                                                                                 421
                                                                                                                                   334
                                                                                                                                                                   361
                                                                                                                                                                                                                        301 ARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA 120
                                                                                                                                                                                                                                                                                      VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                               AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT 180
QPTLPNNSLATPSP-SLPINPGTSHEKHE--
                              KEKĻVDDLĻĀFLĀPITHPERLĢKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD 540
                                                                                                                                                                                                                                                                                                                                                                                                             AHADNVRTKDEINROKOEHVKDNE----KVNSNVAVARSOGRYTTNDGYVFNPADIIEDT
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                                                                                                                                                                   POPAPNIKIDSNSSIVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKOES
                                                                                                                                                                                                                                                                                                                                            GNAYIVPHGGHYHYIPKSDLSASELAAAKAHLAGKNMQPSQLSYSSTASDN------
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                                                                                                                                                                                                        PNGVAI PHGDHYHF I PYSKLSALEEKI ARMVP
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                                                                 KELSSASDGYIFNPK-DIVEETATAYIVRHG
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Pred. No. 3.6e-85;
77; Mismatches 120;
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US-08-961-083-182
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      Matches
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MEDIUM TYPE: Diskette, 3.50

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS Vers

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (301) 309-85
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: BETELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Str
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sin
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CLASSIFICATION: 435
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STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                225
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                                                                                                                    184 YIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVSN
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 304
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                                                                                                                                                                     DNVRTKDEINRQKQEHVKDNB----KVNGNVAVARSQGRYTTNDGYVFNPADIIEDTGNA
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VAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQP 363
                                ----NTQSVAKGSTSKPANKSENLQSLLKELYDSPSAQRYSESDGLVFDPAKIISRTPNG
                                                                 PGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARG 303
                                                                                                    YIVPHGGHYHYIPKSDLSASELAAAKAHLAGKNMQPSQLSYSSTASDN------
                                                                                                                                                                                                                                            DHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKDAAHA
                                                                                                                                                                                                                                                                DHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHA 123
                                                                                                                                                                                                                                                                                                                 LNQHRSQENKDNNRVSYVDGSQSSQKSENLTPDQVSQKEGIQAEQIVIKITDQGYVTSHG
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                                                                                                                                                                                                                                                                                                                                                                                  28.5%; Score 1187.5;
46.3%; Pred. No. 5.5e
ative 72; Mismatches
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US-09-536-784-182
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                                                                                                                 Matches
                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 182:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
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                                                                                                                 257;
 64
DHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHA 123
                                                                 LGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHG
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VAIPHGDHYHFIPYSKLSALEEKIARMVP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.50 inch, 1
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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STATE: Maryland
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                                                                                                           Score 1187.5; DB 4;
Pred. No. 5.5e-84;
72; Mismatches 117;
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SEQ ID NO 5080
LENGTH: 3696
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                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                   ORGANISM: Staphylococcus epidermidis -09-134-001C-5080
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
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larity 18.5%;
Conservative 141
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Pred. No. 0.0054;
1; Mismatches 348; Indels 31
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US-09-134-001C-3159
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                                                                                                                                                                                 Sequence 3159, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,7664
PRIOR PILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
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Best Local Sim.
Matches 189;
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SEQ ID NO 3159
LENGTH: 10182
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3%; Pred. No. 0.055;
126; Mismatches 368; Indels 320
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SEQ ID NO 6
LENGTH: 812
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Giuliano, Kenneth A. APPLICANT: Kapur, Ravi
TITLB OF INVENTION: A System for Ce
FILE REFERENCE: 97-022-L1
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CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
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                                                      PERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAY----
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Best Local Similarity
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FILING DATE: 18-SEP-1989
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                                                                               EIVEVE---EILPE-
AAAIYNRVKGEKRIPLVRLPYMVEH-TVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPN
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                                                                               DDKNEKVEHEIVEVEBILP - - EDKNEKGQHEIVE
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APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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Patent No. 6284480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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  NKDLLCQEQARKLEVLDLNVKS-----SREQLQYVSKSNQEHKKEVEALQLQLVNSSTE
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                                                                                  LESVKSENEKLKNELVLEIEKRKKYETNEAKITTVATDLSQYYRESKEYIASLYEKLDRT
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18.6%;
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Query Match Best Local Similarity 18.6%; Pred. No. 0.017; Matches 182; Conservative 136; Mismatches 357; Indels 301; Gaps 41; Qy 23 GKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYN 70	RESULT 16 US-09-723-820-6 US-09-723-820-6 Sequence 6, Application US/09723820 Patent No. 6468760 GENERAL INFORMATION: APPLICANT: Nislow, Corey APPLICANT: Sakowicz, Roman APPLICANT: Sakowicz, Roman CONTROL SECULT OF INVENTION Antifungal Assay FILE REFERENCE: 1015 CURRENT APPLICATION NUMBER: US/09/723,820 CURRENT APPLICATION NUMBER: 09/541,782 PRIOR APPLICATION NUMBER: 09/541,782 PRIOR APPLICATION NUMBER: 09/541,782 PRIOR FILING DATE: 2000-04-03 NUMBER OF SEQ ID NOS: 10 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 6 LENGTH: 1073 TYPE: PRT ORGANISM: S.pombe US-09-723-820-6	Db 861 NGSQLLDSK6KAIHSNSRSMYDHCLALAESQKQGVNLEVQTLDRLLQKVK 911 Qy 677 HSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEDEVPQVETEKVEAQLKEAEV 736	578 ERNNKENENNFWNLKFNLLTMLRSFHGSFTDETNGYFTLLNDFNASMEELLNTHSN 452 KALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPIT
RESULT 17 US-08-961-083-118 / Sequence 118, Application US/08961083 PACENT NO. 6159469 / GENERAL INFORMATION: APPLICANT: Choi et. al. FITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452 CORRESPONDENCE ADDRESS: ADDRESSE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA ZIP: 20850 COMPUTER READABLE FORM:	Ob 754 VKTCTTSLNDADII-LSDYISDQKSKFESKQQDLIANIGKIVSNFLQEQNESLYTK 808 Oy 579 LPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVK 625	425 LTAKKENVAPRDQEFYDKAYNLLTEAH	Qy 181 GDAYIVPHGDHYHYIPKNELSASELAAABAFLSGRGNLSNSRT

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Best Local 9
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TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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Local Similarity 19.2%; Pred. No. 0.022;
ses 154; Conservative 111; Mismatches 284; Indels 25
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STRANDEDNESS: sir
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-VEVKNGNLIIPHKDHYHNIKFAWFDDHTY-------KAPNGYT-LEDLFATIK-----Y
                                                                TDTAKYFVKVK---
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                                                                                                     KVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHT----
                                                                                                                                             E--ENTETSTQDFQL--EYKKIEIKDIDSVELYGKENDRY-----RRYL---SLSEAP
                                                                                                                                                                                    SQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKE
                                                                                                                                                                                                                             AYVS----AKTOVFHG-DKLVKEVDIENPAKEQVISG-LDYYTPYTVKTHLTYNLGENN
                                                                                                                                                                                                                                                                    AHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPI --- TH-PERLGKPN
                                                                                                                                                                                                                                                                                                               KEVSRTEVA---PVNEVVKVGTLVKVKPTVEITNLTKVEN----KKSITVSYNLIDTTS
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HP Vectra 486/33
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                                                              -SDRFKEMYLPVKS-----ITENTDGTY
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US-09-536-784-118
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Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 154; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 118: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII Text
CURRENT APPLICATION UNMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REGISTRATION NUMBER: 41,971
REGISTRATION NUMBER: 41,971
                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 118:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION TELEPHONE: (301) 309-850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                     153 AVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFL 212
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                                                                                                                                                    76 LKIEGYQYIGYIK-TKKQDNTELSRTVDGKYSAQRDSQPNSTKTSDVVHSADLEWNQGQG 134
SGRGNLSNSRTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLK 272
                                                                 KVSL - - - QGEASGDDG
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COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                            IKVDGKYYV-YLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRND-------G
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CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1040 amino acids
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                                                                                                                                                                                                                                    3.5%; Score 144; DB 4; Length 1040; ilarity 19.2%; Pred. No. 0.022; Conservative 111; Mismatches 284; Indels 25
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SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                     TITLE OF INVENTION: Use of Protein Tyrosine Phosphatase Zeta as a TITLE OF INVENTION: Treatment and Visualization of Brain Tumors FILE REFERENCE: 262/235 AGY CURRENT APPLICATION NUMBER: US/09/816,703A CURRENT FILING DATE: 2001-03-23 NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                          APPLICANT: Melcher, Thorsten APPLICANT: Mueller, Sabine APPLICANT: Chin, Daniel
LOCATION: (1). (2314)
OTHER INFORMATION: Krueger, N.X. and Saito, H.: A human transmembrane protein-tyrosi
OTHER INFORMATION: ne-phosphatase, PTP zeta, is expressed in brain and has an N-term
OTHER INFORMATION: inal receptor domain homologous to carbonic anhydrases; Proc. Nati
OTHER INFORMATION: 1. Acad. Sci. USA 89 (16), 7417-7421 (1992
                                                                                                                                           LENGTH:
                                                                                  FEATURE:
NAME/KEY: Reference
                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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LOCATION: (1)..(2314
OTHER INFORMATION: L
OTHER INFORMATION: n
OTHER INFORMATION: C
                    OTHER INFO
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LOCATION:
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LOCATION: (324)...(324)
OTHER INFORMATION: Glycosylation; N-linked
NAME/KEY: SITE
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LOCATION: (312)..(406)
OTHER INFORMATION: Fibronectin Type-III
NAME/KEY: SITE
NAME/KEY: SITE
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OTHER INFORMATION: Glycosylation;
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: SITE LOCATION: (105)...(105)
OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...)
                                                          LOCATION: (997)..(9
                                                                                                                 OTHER INFORMATION: Splicing
                                                                                                                                                           LOCATION: (677)...(677)
OTHER INFORMATION: Glycosylation;
NAME/KEY: VARSPLIC
                                                                                                                                                                                                                                         OTHER INFORMATION: Chondroitin sulfate (potential)
                                                                                                                                                                                                                                                                                               LOCATION: (629)..(629)
OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                              LOCATION: (602)..(602)
OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: BINDING
LOCATION: (587)..(587)
OTHER INFORMATION: Chondroitin sulfate (potential)
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OTHER INFORMATION: Glycosylation;
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OTHER INFORMATION: Glycosylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (497)..(497)
OTHER INFORMATION: Glycosylation; N-linked
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OTHER INFORMATION: Glycosylation; N-linked
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LOCATION: (134)..(134)
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OTHER INFORMATION: Extracellular (potential)
NAME/KEY: misc feature
LOCATION: (25)..(2314)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION: Levy, J.B., et al.; The cloning of a red INFORMATION: ne phosphatase expressed in the central INFORMATION: Chem. 268 (14), 10573-10581 (1993)
INFORMATION: Glycosylation;
                                                                                                    BINDING
                                                                                                                                                                                                   (677) .. (677)
                                                                                                                                                                                                                                                                                  BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                    (1017) .. (1017)
                                                                                                                                                                                                                                                                  (637)..(637)
                                                                               ) . . (997)
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                                                        Chondroitin sulfate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      By similarity
                                                                                                                     variant;
N-linked (GLCNAC...)
                                                                                                                                                                                N-linked (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-linked
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                                                        (potential)
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(potential)
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OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...)

1308

-PPSP

542

510 1425 459

1596 583

1656

627

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US-09-816-703A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (2222)..(2222)
OTHER INFORMATION: Ancestral active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1998)..(2314)
OTHER INFORMATION: Protein-tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: ACT SITE
LÓCATION: (1932)..(1932)
OTHER INFORMATION: Active site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Protein-tyrosine phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1722)..(1728)
OTHER INFORMATION: Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1636)..(1661)
OTHER INFORMATION: Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
LOCATION: (1617)..(1617)
OTHER INFORMATION: Glycosylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1561)..(1561)
OTHER INFORMATION: Glycosylation; N-linked
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Chondroitin sulfate (potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                      1091 SISSTKGMFPGSLAHTTTKVFDHEISQVPENNFSVQPTHTVSQASGDTSLKPVLSANSEP
                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                        994 GEW----SGASSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169;
                                                                                                                                                                                                                                                                                                                                                           111 GKYYVYLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVAL-----ARSQGRYT 164
                                                                                                                                                                                                                                                                                                                                                                                                954 VGVTYQGSLFSGPSHI-----PIPKSSLITPTASLLQPTHALSG-------D
                                                                                                                                                                                                                                                                                                                                                                                                                                 51 IKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVD
                   DPILVETPKVDKISSTMLHLIVSNSASSENMLHSTSVPVFDVSPTSHMHSASLQGLTISY
                                                         DGLVFDPAQ----
                                                                                            ASSDPASSEMLSPSTQLLFYETSASFSTEVLLQPSFQASDVDTLLKTV--LPA----VPS
                                                                                                                                 SVSNPGTT------NTNTSNNSNTNSQAS-QSNDIDSLLKQLYKLPLSQRHVES
                                                                                                                                                                                                              AFLSGRG--
                                                                                                                                                                                                                                               TSVFGDDNKALSKSEIIYGNETELQIPSFNEMVYPSESTVMPNMYDNVNKLNASLQETSV 1090
                                                                                                                                                                                                                                                                                    T----DDGYIFNASDIIEDTGDAYIVPHGDHYHY-----IPK----NELSASELAAAE 209
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                                                         ---ITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRY 335
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Pred. No. 0.12;
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TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/920,28:
FILING DATE: 13-AUG-1992
                                                                                                                                                                                                                                                                                                                 ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                            CLASSIFICATION: 435
ATTORNBY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DNA Expressi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 703-241-1300
                                                                                                                                                                                                                                                                                                                                                                                        STRIET: P.O. Box 747
CITY: Falls Church
STATE: Viroinia
                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILIYWRKCFQTAHFYLEDSTSPRVISTPPTPIFPISDDVGAIPIKHFPKHVADLHASSGF 1716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAWAVLTSDEESGSGQGTSDSLNENETSTDFSFADTNEKDADGILAAGDSEITPGFPQSP
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                                                         703-241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garoff, Henrik
Liljestrom, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Expression Systems
                                                                                                                                                                                                                                US/07/920,281C
                       2:
                                                                                                                 828-103P
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                                                                                                                                                                                                                                                                    Version
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RESULT 21
US-08-466-277-2
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                                                                                                                            Sequence 2, Application US/08466277
PATENT NO. 6190666
GENERAL INFORMATION:
APPLICANT: Garoff, Henrik
Liljestrom, Peter
TITLE OF INVENTION: DNA Expression Systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 137;
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Best Local Similarity
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1971
                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart,
STREET: P.O. Box 747
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                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                            2086 FAKTHNLVPLQEVP-MDRFTVDMKRDVKVTPGTKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HKALF----XNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAP---ITHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGRAGAYIFSSDTGS---GHLQQKSVRQ----HNLQCAQLDAVQEEKMYPPK---LDTER 1861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AYLASRAAERPVPAPR-KPTPAPRTAFRNKLPLTFGDFDEHEVDALASGITFGDFDDVLR
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                                              Kolasch
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2431 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION UMBER: US/08/466,277
FILING DATE: 06-Jun-1995
CLASSIFICATION: -Unknown>
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NAME: MUTED YT., Gerald M.
REGISTRATION NUMBER: 28, 977
REFERENCE/DOCKET NUMBER: 82.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
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                                                                                                                                   1862
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HWIGKDSLSDKE---KVAAQAYTKEKGI----
                                           RPVYSPTVIERFSSPDVAIAACNEYLSRNYPTVASYQITDEYDAYLDMVD--
                                                                                                                                                                                                                        LGRAGAYIFSSDTGS---GHLQQKSVRQ----HNLQCAQLDAVQEEKMYPPK---LDTER 186:
                                                                                                                                                                                                                                                                                                            AYLASRAAERPVPAPR-KPTPAPRTAFRNKLPLTFGDFDEHEVDALASGITFGDFDDVLR 1811
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                                                                                                                                                                             HKALF-----XNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAP---ITHP
                                                                                                                                                                                                                                                                  ISR----YVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEA
                                                                                                                                                                                                                                                                                                                                                       HWVPDSRPEQPSPQPTPEPSPGPQPAPNLKI-----DSNSSLVSQLVRKVGEGYVFEEKG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                               -SQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSN 338
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                                                                                     ERLGKPNSQIEYTEDEVRIA----QLADKYTTSDGY-IFDEHDIISDEGDAYVTPHMGHS
                                                                                                                                   EKLLLLKMOMHPSEANKSRYOS-RKVENMKATVVDRLTSGARLYTGADVGRIPTYAVRYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
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Pred. No. 0.14;
3; Mismatches 253;
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  ---LPPSP----
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  -DADVKAN----
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US-08-714-741-32
; Sequence 32, A
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Best Local Similarity
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GENERAL INFORMATION:
                                                                                                                                                                       Matches 110;
                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 840-071 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Brooks-Wa
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Frommer Esq., William S. REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 16-SEF
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                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                     3950 GGLEKALTDEKVGLNNTPKALDTAPKALDTALNELGPDGDE
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                                                                                                                                  239
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: New York
                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                PSVSNPGTTNTNTSNNSNTNSQASQSNDIDS----LLKQLYKLPLSQRHVESDGL----
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                                                                                             PGGETPDGLDKEASEDSNIGALPNQVSDLENQVSELDREVTRLPSDLKDTEGNNVGDYVK
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                                                                                                                                                                                                                                                                                                                                         8991 amino acids
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VENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
VENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
VENTION: PORTIONS AND PRODUCTS
EQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                  (212) 840-0712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Crain, Marilyn J.
Hollingshead, Susan
Tart, Rebecca
                                                                                                                                                                       Conservative
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Swiatlo, Edwin
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18.8%; Pred
70;
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                                                        --VFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARI 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                        454312-2460
                                                                                                                                                                                       Score 141; DB Pred. No. 1.1;
                                                                                                                                                                     Mismatches 230; Indels 176;
                                                                                                                                                                                                          DB 4; Length 8991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08976255 Patent No. 6136581
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FRACESQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,255
FILING DATE: No. 6136581ember 21, 19
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                          APPLICATION NUMBER: 60/031,675
FILING DATE: NO. 6136581ember
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                           REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Plowman, Gregory
TITLE OF INVENTION: KINASE GENES AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Calif
                                                          TELEFAX:
                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  633 West Fifth Street
                                                        (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jono,
                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lyon & Lyon
                                                                            (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---NRLPQQQPPKAEKPAPAPKPEQPVPAPGGWSWRILLARPDRLAARQAELA 4089
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; MOLECULE TYPE: US-08-976-255-14
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Best Local S
Matches 168
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736 -VLLAKVTDSSLKANAT
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                                                              EKR-----SEEVPG-----TSPSALVLVQEQPLPEPVLPEQSPAAQDSCLEARKSQPDE 1163
                                                                                                   HSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKEAE-
                                                                                                                                                                                                                                                                      KEKVAAQAYTKE-----KGILPPSPDADVKANP--TGDSAAAIYNRVKGEKRIPLVRLPY 616
                                                                                                                                                                                                                                                                                                                                                    PNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSD
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                       751
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                                                                                                                                                                                                                                                                                                               -------DVHEALLDSLGSH-TP------QKLVP 102:
                                                                                                                                            -ETFTAGSQGSYRD--
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: EYFP-DEVD-MAP4-EBFP construct
US-09-513-783A-22
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SEQ ID NO 22
LENGTH: 1610
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GENERRAL INFORMATION:
APPLICANT: Giuliano, Kenneth A. APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A System for Cel
FILE REFERENCE: 97-022-L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 97-022-L1
CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
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TYPE: PRT
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                     DVAPPMEEEIVPGNDTTSPKETETTLPIKMDLAPPEDVLLTKETELAP---
                                                                                                                                                                                                                                                                                                                                                      LFVSSGPTNASAFTERDNPS----EDSYGMLPCDSF---ASTAVVSQEWSVGAPNSPCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDEKTGNSESKKKPCLD-TSQVEGIPS-SKP-TLLANGDHGMEGNNTAGSPTD---FLEE
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                                                                                                                                          GKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAY-----
                                                                                                                                                                                                                             LLTEAHKALFXNKGRNSDFQALDKLLERLND----ESTNKEKLVDDLLAFLAPITHPERL 501
                                                                                                                                                                                                                                                                                                      EKGISRYVFAKDLPSETVKNLE-----SKLSKQESVSHTLTAKKENVAPRDQEFYDKAYN 445
                                                                                                                                                                                                                                                                                                                                                                                               IPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFE
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                                                                                                     EITKPDVILANVTQPSTESDMFLAQDMELLTGTEAAHANNIILPTEPDESSTK
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                                                                                                                                                                                   ----ALETMAEQTTDVVHSPSTDTTPGPDTEAALAKDIE-----
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                       -AKGMVSLS
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Best Local Similarity

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                                      ; MOLECULE TYPE: US-08-447-031A-2
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Patent No. 5851794
GENERAL INFORMATION:
Query Match
                                                                                                                            TELEFAX: (703) 836-202
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: WO PFILING DATE: 22-OCT-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,804
FILING DATE: 21-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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TITLE OF INVENTION: A COLLAGEN BINDING PROTEIN AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 8
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                                                                        TYPE: ami
TOPOLOGY:
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CITY: Alexandria
""" roinia
                                                                                                                                                                                                                        NAME: McGowan, Malcolm | REGISTRATION NUMBER: 39 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: SE 9003374-7 FILING DATE: 22-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 22 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0
FILING DATE: 22-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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HOOK, Magnus
JONSSON, Hans
LINDBERG, Martin
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P.O. Box 1404
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-- NO: 2:
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 3.3%;
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 Score 136.5;
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                                                                                                                                                                                                       NKYTPETTSISGEKVWDDKDNQDGKRPEKVSVNLLANGEKVKTLDVTSETNWKYEFKDLP
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                                                                                            IMAEAEKLLALLKGSNPSSVSKE 793
                                                                                                                                                                   QV-ETEKVEAQLKEAEVLLAKVTDSSLKANAT-----ETLAGLRNNLTLQIMDNNS 770
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                                                                                                                                KYDEGKKI EYTVTEDH----
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                                                                                                                                                                                                                                          -ASEHVLGKKDHSED--PNK---NFKADEEPVEETPAEPE-----VP 720
                                                         -- QDGKRPTEIKVE 1024
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                                                                                                                                - VKDYTTDINGTTITNKYTPGETSATVTKNWD--
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CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 812
TYPE: PRT
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Best Local
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APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A System for Cell Based
FILE REFERENCE: 97-022-L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: EYFP-DEVD-MAPKDM construct
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VSLSEIEEALAKNDVRSAE-IPVAQ-ETVVSETEVVLATEVVLP-
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                                 ANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDH
                                                                    SSTKDVAPPMEEEIVPGNDTTSPKETETTLPIKMDLAPPEDVLLTKETELAP
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                                                                                                     -VTPHMGHSHWIGKDSLSDKEKVAA------QAYTKEKGILPPSPDADVK 586
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2; Mismatches
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Pred. No. 0.061;
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US-09-513-783A-32
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CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 32
LENGTH: 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Giuliano, Kenneth A.
APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A System for Cell Based Screening
FILE REFERENCE: 97-022-L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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442 KAYNLLTEAHKALFXNKGRNSDFQALDKLLERLND----ESTNKEKLVDDLLLAFLAPITH 497
                                                                                                                                                                                                                                                                                                            299 PLIDGDEKTGNSESKKKPCLD-TSQVEGIPS-SKP-TLLANGDHGMEGNNTAGSPTD---
                                                                                                                                                                                                                                                                                                                                                  211 -FLSGRGNLSNSRTYRRONSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 HYQQNTPIGDGPVLL-----PDNHYLSYQSALSKDPNEKRDHMVLLEFVTAAGITLG
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                                                              SPCSESCVS-----PEVTIETLQPATELSKAAEVESVKEQLPAK
                                                                                                                                                                                                                                                                   LLKQLYKLP---LSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEER
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                                                                                                  YVFEEKGISRYVFAKDLPSETVKNLE-----SKLSKQESVSHTLTAKKENVAPRDQEFYD
                                                                                                                                             LADLLFVSSGPTNASAFTERDNPS----EDSYGMLPCDSF---ASTAVVSQEWSVGAPN
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19.7%;
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Pred. No. 0.093;
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US-08:015-973-1
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Patent No. 5604094
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
                                                        Query Match
Best Local Similarity
                                    Matches 169;
                                                                                                                                                                                                     TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,973
FILING DATE: 10-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                    LENGTH:
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 51 IKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVD 110
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VENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
VENTION: PHOSPHATASE-BETA
                                    Conservative 123;
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                                                        3.2%; Score 134; DB
19.2%; Pred. No. 0.46;
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                                    Mismatches 276;
                                                                       DB 1; Length 2308;
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                                    Indels 310;
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                                    Gaps
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                                                                     Sequence 1, Application US/08448164
Patent No. 5925536
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-BETA
NUMBER OF SEQUENCES: 9
                                                        CORRESPONDENCE ADDRESS:
                   STREET:
                                      ADDRESSEE:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-021
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FILING DATE: 10-FEB-1993
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TOPOLOGY: linear
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                                                         SVPIGNGHVAITAVSPHRDGSVTSTKLLFPSKATSELSHSAKSDAGLVGGGEDGDTDDDG 1425
                                                                                                                                    RHVFATPVLSIDEPLNTLINKLIHSDEI---LTSTKSSVTGKVFAGIPTVASDTFVSTDH
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Matches 169;
                    Query Match
Best Local Similarity
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APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,929
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: A NEW CLASS OF RPTPASES: THEI
TITLE OF INVENTION: STRUCTURAL DOMAINS AND LIGANDS
                                                                                               MOLECULE TYPE:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                 NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30742 REFERENCE/DOCKET NUMBER: 7
                                                                                                                 STRANDEDNESS: sing TOPOLOGY: unknown
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TELEFAX: 212 869-8864/9741
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CLASSIFICATION:
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STATE: New York
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5. 6160090
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Barnea, Gilad
Conservative 123;
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                    3.2%; Score 134; DB
19.2%; Pred. No. 0.46;
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  Mismatches
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                                    Length 2308;
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51 IKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVD 110

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US-09-599-652-2
                                                                                                                                               Sequence 2, Application US/09599652
Patent No. RE37741
GENERAL INFORMATION:
                                                                         APPLICANT:
                     TITLE OF INVENTION:
                                                          APPLICANT:
                                                                                                              APPLICANT:
   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                       1597
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 BENDEL, CATHERINE M.
TAO, NIAN-JUN
KENDRICK, KATHLEEN
IVENTION: CANDIDA ALBICANS GENE,
IVENTION: PROTEIN, ANTIBODIES, AI
EQUENCES: 12
                                                                                                            GALE, CHERYL A.
                                                                                                                                    HOSTETTER, MARGARET
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; MOLECULE TYPE:
US-09-599-652-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 612-305-1228 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 03-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: MUETING, ANN
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEPHONE: 612-305-1217
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ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH,
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MINNEAPOLIS
STATE: MINNESOTA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/599,652 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM:
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AYNLLTEAHKALFXNKGRNSDFQALDKLLER-LNDESTNKEKLVDDLLAFLAPITHPERL 501
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                                                                                                                                  LNSASQSQISLNALEKQRQTQEQEQTQAAEPEEETSFSDNIKVKQEPKSNLEFVKVTIKK
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                                                                                           VGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDK 442
                                                                                                                                                                   IPLRYRS----NHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKI----DSNSSLVSQLVRK 382
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.3;
28; Mismatches
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Patent No. 5886151
   Query Match
                                                                                                   TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: HOSTET
                                                                                                                                                                                      CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MUETING, ANN M.
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MIETING, RAASCH, GEBHARDT & SCHWAPPACH,
STREET: 119 NORTH FOURTH STREET, SUITE 203
                                                                                                                                         TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: CANDIDA ALBICANS GENE, IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
                                                      TOPOLOGY:
                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                             STATE: MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                            CITY: MINNEAPOLIS
                                                                                          ENGTH:
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  Score 133.5;
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                                               Sequence 2, Application US/09264604
Patent No. 6346411
GENERAL INFORMATION:
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HOSTETTER, MARGARET K. GALE, CHERYL A. BENDEL, CATHERINE M. TAO, NIAN-JUN
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112 KYYVYLKDAAHADNVRTKEEINRQKQ---EHSQHREGGTPRNDGAVALARSQGRY--TTD
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846 PRSFTPLSTKNVLSNIDNDPNVVEPPEPKSYAEIRNARRLSANKAAPN
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1664 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 0 FILING DATE: 03-MAY-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KENDRICK, KATHLEEN
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CITY: MINNEAPOLIS
STATE: MINNESOTA
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STRANDEDNESS: si
TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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VGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDK
                                                      LNSASQSQISLNALEKQRQTQEQEQTQAAEPEEETSFSDNIKVKQEPKSNLEFVKVTIKK
                                                                                                                             SRDKLETTKEHDAPEHNNENFIDAKSTNTNKGQLLVSSDDHLDSFDRS-YNHTEQSILNL
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                                                                                                                                                                                                                                                                                                          DGYIFNASDI---IEDTGDAYIVPHGDHYHYI-----PKNELS--ASELAAAEAFLSGR
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                                                                                         IPLRYRS----NHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKI----DSNSSLVSQLVRK
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612-305-1228
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17.9%;
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Pred. No. 0.3;
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; APPLICANT: Meyer, Th
; TITLE OF INVENTION:
;NEGATIVE HOST CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 183; Conserv
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 01-JUL-1987
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                                                                                                                                                                DAHFSKNNEVVFEDDWINRTFKÅAEIAVNOSASFSSGRNVDDITANITATDNAKVNLGYK
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                    IQGQGNSRVSLNQHSKWHLTGDSQVHNLSLADSHIHLNNASDAQSANKYHTIKINHLSGN 863
                                                        ---QSNDIDSLLK-----QLYKLPLSQRHV-----
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                                                                                             --NGDEVCVRSDYTGYVTCNTGNLSDKALNSFDXATKINGNVNLNQNAALVLGKAALWGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.2%; Score 132.5; Dilarity 18.1%; Pred. No. 0.31; Conservative 125; Mismatches
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US-09-457-708-2; Sequence 2, Application US/09457708; Patent No. 325483;
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APPLICANT: Povey, Sue
APPLICANT: Povey, Sue
APPLICANT: Halley, Sicky
TITLE OF INVENTION: Compositions and N
TITLE OF INVENTION: Sclerosis-1 (TSC-1
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEULIA Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,708
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                             COUNTRY: U.S.
ZIP: 20004-1008
                                                                                                                                                                                               CITY: Washington
     FILING DATE
                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                  b.C
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1455 Pennsylvania /
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 639-6604
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: not relevant MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: SANTO, Michael A.
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: no
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NLESKLSKQESVSHTLTAKKENVAPR---PQEFY-DKAYNLLTEAHKALFXNKGRNSDFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KPGHVAEV---YLVHLHASVYALFHRLYGMYPCNFVSFLRSHYSMKENLETFEEVVKPMM
                                                   WKV----SLQKEQARYNQLQEQRDTMVTKLHSQIRQLQHDREEFYNQSQELQTKLEDC--
                                                                                                                          LLYERFKRQQHALRNRRLLRKVIKAAALEEHNAAMKD-----
                                                                                                                                                             -IYNRVKGEKRI------PLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHT
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Pred. No. 0.22;
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US-09-950-046A-2
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                         -09-950-046A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 639-659
TELEFAX: (202) 639-6604
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: not relevant MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/950,046A
FILING DATE: 12-Sep-2001
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Vinson & Elkins
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO:
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                                                                                                                                                                                                                                                                                  al Similarity
155; Conserv
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                                                                                                                                                                     EHSQ-HREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT----GDAYIVPHGDHY 192
                                                                                            HYIPKNELSAS-ELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVSNPG-TTNTN
                                                                                                                                EHVRIHPELVTGSKDHELD-PRRWKRLETHDVVIECAKISLDPTEASYEDGYSVSH----
                                                                                                                                                                                                         KPGHVAEV---YLVHLHASVYALFHRLYGMYPCNFVSFLRSHYSMKENLETFEEVVKPMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRQLLVLGEVNELYLEQLQNKH--SDTTKEVEMMKAAYRKELEKNR 892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1164 amino acids
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larity 18.8%;
Conservative 122
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                                                       -QISARFPHRSADVTTSPYADTQNSYGCATSTPYSTSR---LMLLNMPGQLPQTL
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ley, Dicky
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                                                                                                                                                                                                                                                                              Score 132; DB Pred. No. 0.22; Pred. No. 0.22; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 644804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 458, Application US/09071035
                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.
FILING DATE:
                       ATTORNEY/AGENT INFORMATION: NAME: A. Anders Brookes
                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gil H.
                                                                                                                                                                                      COMPUTER: HP Vectra
OPERATING SYSTEM: MS
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                     STREET: 9410 Ker
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                  COUNTRY: U
                                                           FILING DATE
                                                                                                               CLASSIFICATION:
     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 849 NRQLLVLGEVNELYLEQLQNKH--SDTTKEVEMMKAAYRKELEKNR 892
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 458:
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LENGTH: 2032 amino aci
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                                                                                                                                                                                           --VTEDGTITPDKSVILEEGKDYTLE-----VTTDNETGQQKIVVKMAHIEAPYYMEY 1041
                                                                                                                                                                                                                           KYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVA-----AQAYTKE
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                                                                                                                                                                                                                                                                                            -----EKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLAD
                                ---TI-----KYYVEHPDERPHSNDGWGNASEHVLGKKDHS 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 132;
Pred. No. 0.
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Best Local
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APPLICANT: Gil H. Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (301) 309-85 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: A. Anders Brookes
REGISTATION NUMBER: 36,373
REFERENCEIDOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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OPERATING SYSTEM: MSDOS version 6.2
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                                  GAV-----DY-----QNSTIGWTLAV---
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RESULT 39
US-09-071-035-466
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                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: En
                                                                             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA
                      FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                     ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                  ZIP: 20850
                                                                                                                                                                                                                                 COUNTRY:
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NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 466:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.2%; Score 132; DB 4; Length 2032; Best Local Similarity 19.5%; Pred. No. 0.54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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TOPOLOGY: lir
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1102
                                                                                 1042 RSLVTSSAAGSTDTVSNQVSITGNGSEVVHGDDNGDVVVDIDHSGGHATGTKGKIQLKKT 110
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                                                                                                                                                                                                                                                                                                                                                                                      TLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNK--
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AMDETTILAGAHFQIMDQAKTQVLREGTVDATGVITFGGLPQGQYILVETKAPEGYTVSD 116:
                                          YMVEHTV------KAPNGYTLED
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                                                                                                                                                                      --VTEDGTITPDKSVILEEGKDYTLE-----VTTDNETGQQKIVVKMAHIEAPYYMEY 104:
                                                                                                                                                                                                             KYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVA-----
                                                                                                                                                                                                                                                          EYHKDDPDHVYWHVMINGAQSVLDDVVITDTP--SPNQVLDPESLVIYGTN
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                                                                                                                              KGILPPSP--DADVKANP---TGDSAAAIYNRVKGEKRIPL---
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PCT-US93-03077-1
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Best Local S
Matches 141
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                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1093 amino acids
                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: April 2, 199
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: PROPERTY PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wu, FOON KIN
TITLE OF INVENTION: PROTEIN CELLULAR FACTOR USEFUL FOR
TITLE OF INVENTION: REGULATING GENE EXPRESSION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: UTI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1540
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                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                 TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 713-749-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kammerer, Patricia A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Houston
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STREET: P.O. Box 4433
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    182
                                        225
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                                                                                                                                                                                                                  Similarity
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                                        IALEPKEQKHEDRQSNTP---SPPVSTFSSGTSTTSDIEVLDHESVISESSASSRQETTD
                                                                             EINROKQEHSOHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTG--
                                                                                                                  HEETVNKESDMKVPTVSLKVSESVIDVK------TTMESISNTSTQSLTAETKD
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Gaynor, Richard B.
                                                                                                                                                                                                  Conservative 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19930331
                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                3.1%; Score 131; DB 16.7%; Pred. No. 0.24;
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  -- DAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRR 226
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                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                   DB 5; Length 1093;
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                                                                                                                                                                                              Indels 216;
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                                                                                                                SOFTWARE: PatentIn
SEQ ID NO 49
LENGTH: 968
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Ole THASTRUP, et al.
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating
TITLE OF INVENTION: On A Cellular Response
                                                                                                                                                                                                                                                                                                                               Sequence 49, Application US/09417197
Patent No. 6518021
                    OTHER INFORMATION: EGFP-p85alpha fusion -09-417-197-49
                                                                                                                                                                     FILE REFERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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To An

Query Match

Local Similarity

Length

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RESULT 42
US-09-324-867-5
; Sequence 5, Application US/09324867A
; Patent No. 6251632
; GENERAL INFORMATION:
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APPLICANT: Lillicrap, David
APPLICANT: Cameron, Cherie
APPLICANT: No. 6251632ley, Colleen
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17.0%; Pred. No. 0.22;
ative 105; Mismatches 253;
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APPLICANT: Horrocks, L. Suzanne Hoyle
APPLICANT: Hough, Christine
TITLE OF INVENTION: Canine Factor VIII Gene, Pri
FILE REFERENCE: 1669.0010002/JAG/BJD
CURRENT APPLICATION NUMBER: US/09/324,867A
CURRENT FILING DATE: 1999-06-03
EARLIER APPLICATION NUMBER: 09/035,141
EARLIER APPLICATION NUMBER: 60/039,953
EARLIER FILING DATE: 1998-03-069
EARLIER FILING DATE: 1997-03-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 2115
TYPE: PRT
ORGANISM: Sus spp.
US-09-324-867-5
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Matches 141; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 RNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAA
                                                                                                                                                                                                                                                                                                                                                      DGYIFDEHDIISDEGDAYVTPHMGH-SHWI----GKDSLSDKE------
AVPRRRVKQSLKQIRLPLEEIKPERGVVLNATSTRWSESSPILQGAKRNNLSLPFL 1254
                                                                                                                                                                                                                                                                                                                                                                                                    ASLTKDDVLFKVNIS----LVKTNKARVYLKTNRKIHIDDAALLTENRASATFMDKNTTA 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAP
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                                     QVETEKVEAQLKEAEVLLAKV-TDSSLKANATET-----LAGL-RNNLTLQIM 766
                                                                                                                                                                                                                                       GQSSGQGRIRVAVEEEELSKGKEMMLPNSELTFLTNSADVQGNDT------HSQGKK
                                                                                                                                                                                                                                                                               -----KVAAQAYTKEKG---ILPPSP-----DADVKANPTGDSAAAIYNRVKGEK 607
                                                                                                                                                                                                                                                                                                                      SG------LNHVSNWIKGPLGKNPLSSERGPSPELLTSSGSGKSVK 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                         EKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSP-----GPQPAPNL-KIDSNSS
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                                                                                                                  YYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKA--DEEPVEETPAEPEVP----
                                                                                                                                                          SREEMERREKLVQEKVDLPQVYTATGTKNFLRNI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDQ------EFYDKAYNL--LTEAHKALFXNKGRNSDFQALDKLLERLNDESTNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----ARNEADDYLPGARERNTAPSAAARLRPELHHSAERVLTPEPEKELKKLDSKMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLLKQLYKLPLSQRHVESDGLVF---DPAQITSRTARGVAVPHGDHYHFIPYSQMSELEE 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNRGMTALLKV---YSCD-----RDIGDYY----DNTYEDIP-----
                                                                             -HAPVPQDSRSLNDSAERAETHI--
                                                                                                                                                                                               -RIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIK 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.1%; Score 130; DB 3; 19.7%; Pred. No. 0.82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84; Mismatches 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SPTIPSDT-----LSAETERTHSLGPPHPQVNF
                                                                             -----AHFSAIREEAPL-EAPGNRTGPGPRS 1198
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GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5095:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature LOCATION: (B) LOCATION 1...525 SEQUENCE DESCRIPTION: SEQ ID NO: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID
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                                                                                                               183
                                                                                                                                                                                        126 VRT---KEEINROKOEHSOHREGGTPRNDGAVALARSOGRYTTDDGYIFNASDIIEDTGD 182
                                  243 NPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTAR
                                                                                                                                                   209 ATAEDKKADLNROKAE-AEAEQARIREQQRLAEQARQQAAQ-----
                                                                                                                                                                                                                                    160 KAVEDKKAENDAKLKE---
                                                                                                                                                                                                                                                                                                             108
  296 QSSATEESTTPESSTEESTA---
                                                                                                                                                                                                                                                                     66 YHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHADN 125
                                                                                                                                                                                                                                                                                                                                                                                          93;
                                                                                                                                                                                                                                                                                                                                                8 QARTVKENNRVS-YIDGKQATQKTENLTPDEVSKREG-INAEQIVIKITDQGYVTSHGDH
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                             AYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVS 242
                                                                                                                                                                                                                                                                                                           QAREAQVSNTSSNYIDAV-----LNADSLADAIGRVQAMTTMVKANNDLMEQQKQDK 159
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ZIP: 02354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: CD/ROM ISO9660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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21.1%;
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Pred. No. 0.098
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
-----PESSATEES----TTAPESSATEE
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US-08-826-267-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: AMY E. MAIDERGOUESE
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DEF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
PRIOR APPLICATION DATA: 60/014,2
APPLICATION UNMBER: 60/014,2
FILING DATE: 27 MARCH (1996)
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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STREET: 20
STREET: 20
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                    147 TPRNDGAVALARSQG---RYTTDDGYIFNASDI---IEDTGDAYIVPHGDHYHYIPKNEL
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                                                                                                                                                                                                                                                                                                                                              H: 2860 amino acids amino acid
NLLPKVS-----TMLDRLHSTRQHLHQMWHVRKLKLDQCFQLRLFEQDAEK---MFDWI
                                                                           NWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSL-LKQLYKLPLSQRHVESDGLVFD--
                                                                                                         -PQDLEGARNMIEEHSQLKKKVIKAPIEDLDLEGQKLLQRIQSSESFPKKNSGSGNADLQ
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(617)227-5941
--- TD NO: 2:
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Streuli, Mo. 5994070el TRIO Molecules and Uses Related Thereto
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Pred. No. 1.6;
08; Mismatches
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                                                                                                                                                                                                                                                               Length 2860;
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RESULT 45
US-08-188-228-48
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       APPLICATION UNMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474.6300
                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/188,228
                                                                                                                                                                                                                                                                                                                                                          ZIP: 60606
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND
                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TELEPHONE:
                                                                                                                                                                                                                                           FILING DATE:
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                                                                            RESULT 46
US-08-332-643-42
; Sequence 42, Application U; Patent No. 5639634; GENERAL INFORMATION: Suzuki, Shi
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Best Local Similarity
Matches 132; Conserv
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                                                APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: CADHERII NUMBER OF SEQUENCES: 56
                CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall,
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                Marshall,
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                                                 CADHERIN MATERIALS
56
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                 O'Toole,
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Pred. No. 0.28;
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                 Gerstein,
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US-08-332-643-42
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Best Local Similarity
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 916 amino acids
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APPLICATION NUMBER:
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REFERENCE/DOCKET NUMBER: 27866
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                      QAYTKEKGILPPSPD-----
                                                                                                                                       DSTTANGMVRYRIVTQTPQSPSQNMFTINSETGD-IVTVAAG---W-----DREKV--
                                                                                                                                                                       KYTTSDGYI-----FDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAA 569
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                                LVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVE
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19.9%; Pre
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Pred. No. 0.28;
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/ MOLECULE TYPE: protein
US-08-332-638-48
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US-08-332-638-48
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                                                                                                                                                                         Matches 132;
                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
LENGTH: 916 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Gr
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                              TYPE:
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Pred. No. 0.
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US-08-296-791-6
US-08-296-791-6
; Sequence 6, Application US/08296791
; Patent No. 6245337
; GENERAL INFORMATION:
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                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
REFERENCE/DOCKET NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-59941/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                    APPLICATION NUMBER: US/01
FILING DATE: 25-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 9
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                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
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                                                                                   NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,801
                                                                                                                                                                                                                                                                                                            ZIP:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1848 emino acids
TYPE: amino acid
TOPOLOGY: unknown
-08-296-700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 18.6%; Pred. No. 0.86 Matches 161; Conservative 109; Mismatches
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                                                                                                                                                                                                                                                                    VAKE---DQPTVEANTQTNEATQSEGKTEETQTAETKSEPT-ESVTVSENQ------
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                                                                                                                                           PDERPHSNDGWGNASEHVLGKKDH-----SEDPNKNFKADEE---PVEETPAEPEVPQV 722
                                                                                                                                                                                                                                                                                                                                            -----NPNSESVPSETTEKVAENPPQ------ENETVAKNEQEATEPTPQNGE--- 1128
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                                                                                                                    PEEVPTDT----NAEEAQALQQTQPTTVAAAETTSPNSKPAEETQQPSEKTNAEPVTPVV 127
                                                                                                                                                                                                                              VRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEH
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18.6%; Pred. No. 0.86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 161;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: FP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
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APPLICATION NUMBER: 1
FILING DATE: 25-AUG-
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APPLICATION NUMBER: PC'
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CITY: San Francisco
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94111-4187
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TGEPNHNELTLFDASNATRNNLEVTLANGSVDRGAWKYKLRNVNGRYDLYN--
                              HVE----SDGLVFDPAQITSR----TARGVAVPHG----
                                                                                              DNTSRTNWVPSVSNPGT-----TNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQR 282
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                                                                 -NTLTVN---SLSGNGSFYYWVDFTN-NKSNKVVVNKSATGN
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4 Embarcadero Center, Suite 3400
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Pred. No. 0.86;
9; Mismatches 271;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 176
LENGTH: 783
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-513-783A-176
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APPLICANT: Giuliano, K
APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A
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                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                               Query Match
Best Local
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CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
                                                                                                                                                                                                                                                                                               Local Similarity
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218 LSNSRTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    612 VRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          556 IGKDSLSDKEKVAAQAYTKE----KGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPL
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                                                                                                                                                                                                       78
                                                                                                                                                                                                                                         62 HGDHYHYYNGKVPYDAIISEELLMKDP-NYKLKDE-----DIVNEVK-GGYVIKVDG--
                                                         -----PDNHYLSTQSALSKDPNE-
                                                                                          RSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGN
                                                                                                                                                                ------KYYVYLKDAAHADNVRTKEEINRQKQEHS----QHREGGTPRNDGAVALA 157
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Дb	Qγ	Db	8	DЬ	Ş	Ф	Ş.	DЪ	Ş	DЬ	ν,	DЬ	δ	DЬ	δ	DЬ	8	DЬ
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Search completed: November 14, 2003, 10:38:25 Job time: 52 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 10
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Maximum DB
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      Published_Applications_AA:*
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Sequence 56, Appl Sequence 194, Appl Sequence 8, Appli Sequence 66, Appl Sequence 383, App Sequence 380, App Sequence 380, App Sequence 376, App Sequence 376, App Sequence 377, App Sequence 377, App Sequence 6, Appli Sequence 3, Appli Sequence 24, Appli Sequence 24, Appli
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RESULT 1
US-09-765-272-56
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GENERAL INFORMATION:
                                                                                                                                       Query Match
Best Local (
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                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 3P340P2
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 08/961,083
FILING DATE: <UNknown>
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
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                                                                                                                     tch 100.0%;
al Similarity 100.0%;
796; Conservative 0;
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          SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA
                                                                TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                              LENGTH: 796 amino acids
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TELEFAX: (301) 309-8512
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1 US-09-815-242-12955
1 US-09-815-242-12955
2 US-10-172-502-14
2 US-10-037-182-16
2 US-10-037-182-14
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US-09-815-242-12996
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Pred. No. 1.2e-291;
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Sequence 12996, A
GENERAL INFORMATI
Sequence 4, Appli
Sequence 5834, Ap
Sequence 12955, A
Sequence 11, Appl
Sequence 14, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 12, Appl
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Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
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US-09-884-465A-7
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US-09-884-465A-7
                                                   PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
                                                                                                                       APPLICANT: Charland, Nathalie
APPLICANT: Charland, Natharine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
                         LENGTH: 840
TYPE: PRT
           ORGANISM: Streptococcus
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Best Local S
Matches 616
                                                                       Sequence 194, Application US/09769787 Publication No. US20030091577A1 GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PMC/P21129WO
CURRENT APPLICATION NUMBER: US/09/769,787
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Pred. No. 2e-223;
5; Mismatches 104;
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PRIOR APPLICATION NUMBER: GB 98
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 194
LENGTH: 826
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                                   KANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGS
                                                                                                              YTLEDLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKP
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Pred. No. 6.4e-193;
3; Mismatches 139;
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
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APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
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TYPE: PRT
ORGANISM: Streptococcus
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                         DSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAP
                                                                         PRDITSDEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEA
                                                                                                                                                                             LNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFD
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KGAEAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAP
                                                                                                                  EHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTG
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                                                                                                                                                        LKDVSSDKVKLVDDILAFLAPIRHPERLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFD
                                                                                                                                                                                                                                       KLAKQESLSHKLGAKKTDLPSSDREFYNKAYDLLARIHQDLLDNKGRQVDFEVLDNLLER
                                                                                                                                                                                                                                                                                                                                                                                                    TARGVAVPHGNHYHFIPYEOMSELEKRIARIIPLRYRSNHWVPDSRPEQPSPOSTPEPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGDAYIVPHGDHYHYIPKNELSASELAAAEAYWNG-----KQGSRPSSSSSYNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.0%; Score 2750.5; DB 11 64.5%; Pred. No. 1.1e-189; tive 90; Mismatches 145;
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID

US-09-765-272-66
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US-09-765-272-66
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Patent No. US20020061545A1
GENERAL INFORMATION:
                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                                                    Local Similarity
nes 519; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 763 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae
122
                               120
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                                                                 62
                                                                                                   60
                                                                                                                                                  1 SYELGLYQARTV-KENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYV 59
                                                             TSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKD 119
                     AAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIED 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGYSLEDLLATVKYYVEHPNERPHSDNGFGNASDHVRKNKADQDSKPDEDKEHDEVSEPT
AAHADNIRTKEEIKRQKQERSHNHNS----RADNAVAAARAQGRYTTDDGYIFNASDIIED
                                                                                                                                    SYELGRHQAGQVKKESNRVSYIDGDQAGQKAENLTPDEVSKREGINAEQXVIKITDQGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/765,272 FILING DATE: 22-Jan-2001
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                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                    77;
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Pred. No. 1.8e-182;
                                                                                                                                                                                                       Mismatches
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APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILLE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-66-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR APPLICATION NUMBER: 50/212,683
PRIOR PILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-884-465A-383
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Unknown Organism
NAME/KEY: MISC FEATURE
LOCATION: (1)...(1)
OTHER INFORMATION: Xaa = Methionine or nothing
NAME/KEY: MISC FEATURE
LOCATION: (557)...(557)
OTHER INFORMATION: Xaa = Glycine or nothing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 383, Application US/09884465A Publication No. US20030077293A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
                                                                                                                                                                                       TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEETPREEKPQSEKPESPKPTEEPEESPEESEEPQVETEKVEEKLREAEDLLGKIQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPAQPRLSENHNLTVTPTYHQ-NQGENISSLLRELYAKPLSERHVESDGLIFDPAQITSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVXSDKVKLVXDILAFLAPIRHPERLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YTLEDLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKP
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                                                                                                           Sequence 382, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptcoccus Antigens
FILE REFERENCE: 055190-0044
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
INUMBER OF SEO IN NOS. 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: MISC FEATURE
; LOCATION: (558) . (558)
; OTHER INFORMATION: Xaa =
US-09-884-465A-383
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
US-09-884-465A-382
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Best Local S
Matches 366
                  NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 382
LENGTH: 1365
TYPE: PRT
  ORGANISM: Artificial Sequence
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Local Similarity 64.9%;
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3; Mismatches 101;
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APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION UNMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
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US-09-884-465A-380
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LOCATION: (557). (557)
OTHER INFORMATION: Xaa = G
NAME/KEY: MISC FEATURE
LOCATION: (558). (558)
OTHER INFORMATION: Xaa = P
JS-09-884-465A-382
                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                            Seguence 380, Application US/09884465A Publication No. US20030077293A1
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NAME/KEY: MISC_FEATURE
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PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 380
LENGTH: 1139
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                              LQIMDNNSIMAEAEKLLALLKGSNPSSV 790
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:||||||:||||||||||: |:|||||: |:|||||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: ||||: ||||: ||||: ||||: ||||: |||: |||: |||: |||: |||: |||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
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Pred. No. 1.4e-120;
Pred. Mismatches 107; I
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RESULT 9
US-09-884-465A-378
; Sequence 378, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee

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Best Local Similarity
Matches 345; Conserv
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SEQ ID NO 378
LENGTH: 1378
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APPLICANT: Onellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
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OTHER INFORMATION: Xaa = Methionine
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                                  LQIMDNNSIMAEAEKLLALLKGSNPSSV 790
                                                                      TEETEEEAEDTTDEAEIPQVENSVINAKIADAEALLEKVTDPSIRQNAMETLTGLKSSLL
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LGTKDNNTISAEVDSLLALLKESQPAPI 568
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Matches 314
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SEQ ID NO 381
LENGTH: 1238
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
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NAME/KEY: MISC_FEATURE
LOCATION: (1)...(1)
OTHER INFORMATION: Xaa = Methionine
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                                    WGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKE 733
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                                                                                                              VEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDG
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FGNASDHVXXNMQPSQLSYSSTASDNNTQSVAKGSTSKPANKSENLQSLLKE
                                                                                                                                                    SEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYT
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Martin, Denis
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Pred. No. 4.2e-111;
7; Mismatches 97;
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APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-004
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 376
LENGTH: 999
TYPE: PRT
ORGANISM: Artificial Sequence
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; Sequence 376, Applic.
; Publication No. US20
; GENERAL INFORMATION:
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OTHER INFORMATION: Unknown Organism
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(1)
OTHER INFORMATION: Xaa = Methionine of
NAME/KEY: MISC_FEATURE
LOCATION: (430)...(430)
OTHER INFORMATION: Xaa = Glycine or no
NAME/KEY: MISC_FEATURE
LOCATION: (431)...(431)
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Best Local
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APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
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326; Conserv
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                                       WGNASEHVLGKKDHSEDPNKNFKADEEPVEETPA------
                                                                                                                                                          SEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYT
                                                                                                                                                                                               SDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHT
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  FGNASDHV--XXDLTEE---QIKAAQKHLEEVKTSHNGLDSLSSHEQDYP--
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o. US20030077293A1
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FEATURE:
OTHER INFORMATION: Unknown Organism
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(1)
OTHER INFORMATION: Xaa = Methionine o:
NAME/KEY: MISC_FEATURE
LOCATION: (570)..(570)
OTHER INFORMATION: Xaa = Glycine or r
NAME/KEY: MISC_FEATURE
LOCATION: (571)..(571)
OTHER INFORMATION: Xaa = Proine or n
US-09-884-465A-377
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PRIOR ETILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 377
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Best Local Similarity
Matches 307; Conserv
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APPLICANT: Owellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-004
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
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812
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Martin, Denis
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Pred. No. 4.3e-110;
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Sequence 6, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
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US-09-884-465A-6
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
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Best Local Similarity
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CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
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 DESGFVMSHGDHNHYFFKKDLTEEQIKAAQKHLEE--
                                  EGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTG-DSAAAI
                                                                         QPTLPNNSLATPSP-SLPINPGTSHEKHE-
                                                                                                          KEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD
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Pred. No. 4.6e-81;
5; Mismatches 180;
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APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PMC/P21129WO
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR FILING DATE: 1999-03-27
PRIOR FILING DATE: 1999-03-19
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SOFTWARE: PatentIn Ver. 2.1
SEQ_ID_NO_38
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Best Local Similarity
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----LTTSKELSSASDGYIFNPK-DIVEETATAYIVRHG--DHFHYIPK-----SNQIG
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45.8%; Pred. No. 2e-78;
htive 77; Mismatches 1
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US-09-769-744A-24
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Best Local Sim
Matches 259;
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PRIOR APPLICATION NUMBER: GB 9816336.3
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/125329
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CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: PCT/GB99/02452
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: GB 9816336.3
PRIOR FILING DATE: 1998-07-27
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APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21122WO
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NUMBER OF SEQ ID NOS: 196
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TYPE: PRT
ORGANISM: Streptococcus pneumoniae
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45.8%; Pred. No. 2e-78;
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US-09-765-272-182
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 182:
US-09-765-272-182
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INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 257; Conserv
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/961,083 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 KEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD 540
                                                                                YIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVSN 243
                                                                                                                                                                                                                                                 DNVRTKEEINROKQEHSOHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                           DHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHG 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNQHRSQENKDNNRVSYVDGSQSSQKSENLTPDQVSQKEGIQAEQIVIKITDQGYVTSHG
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YIVPHGGHYHYIPKSDLSASELAAAKAHLAGKNMQPSQLSYSSTASDN--
                                                                                                                                                                                               DNVRTKDEINRQKQEHVKDNE----KVNSNVAVARSQGRYTTNDGYVFNPADIIEDTGNA
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STRANDEDNESS: single
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
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46.3%;
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APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 384
LENGTH: 913
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US-09-884-465A-384
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                                                                                                                         Matches 189;
                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                 LOCATION: (344)...(344)
OTHER INFORMATION: Xaa = Glycine or nothing
NAME/KEY: MISC FEATURE
LOCATION: (345)...(345)
OTHER INFORMATION: Xaa = Proline or nothing
                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Unknown Organism
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(1)
OTHER INFORMATION: Xaa = Methionine or nothing
                                                                                                                                                                                                                                                              NAME/KEY: MISC FEATURE LOCATION: (344)..(344)
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                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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                   TPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGE 606
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TPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAA
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Martin, Denis
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                                                                                                                         45; Mismatches
                                                                                                                                        Score
Pred.
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1e-62;
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                                                                                                                         Indels 37;
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US-09-884-465A-379
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 YYVEHPNERPHSDNGFGNASDHVRKNKADQDSKPDEDKEHDEVSEPTHPESDEKENHAGL
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; OTHER INFORMATION: Xaa US-09-884-465A-379
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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OTHER INFORMATION: Xaa = NAME/KEY: MISC FEATURE LOCATION: (345)...(345)
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TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 06/212,683
PRIOR FILING DATE: 2000-06-20
PRIOR PILING DATE: 2000-06-20
PRIOR PILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Unknown Organism NAME/KEY: MISC FEATURE LOCATION: (1)...(1)
OTHER INFORMATION: Xaa = Methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                487 DLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYV
YYVEHPDERPHSNDGWGNASEHVLGK-----KDHSE-----
                                                                                        KRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWEDDHTYKAPNGYTLEDLFATIK 666
                                                                                                                                                               TPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAA 121
                                                                                                                                                                                                                                                          DILAFLAPIRHPERLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEGDAYV
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                                                                 KKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGYSLEDLLATVK 181
                                                                                                                                                                                                       TPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGE
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Martin, Denis
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o. US20030077293A1
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Pred. No. 1.5e-62;
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US-09-884-465A-10
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SEQ ID NO 10
LENGTH: 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09884465A Publication No. US20030077293A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/884,465A CURRENT FILING DATE: 2001-06-20 PRIOR APPLICATION NUMBER: 60/212,683 PRIOR FILING DATE: 2000-06-20 NUMBER OF SEQ ID NOS: 384
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APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
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                                     NKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVR
                                                                             YPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEG---NKVY---TGEELTNVV
                                                                                                                                                                                         GPQPAPNLKIDSNSSLVSQLVRKVGE--GYVFEEKGISRYVFAKDLPSETVKNLESKL--
                                                                                                                                                                                                                                 DESGFVMSHGDHNHYFFKKDLTEEQIKAAQKHLEEVKTSHNGLDSLSSHEQDYP-----
                                                                                                                                                                                                                                                                     TARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSP
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Martin, Denis
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   --NNQNFTLANGQKRV----SFSFPPELEKKLG--
                                                                                                                 -SKQESVSHT----LTAKKENVAPRDQEFYDKAYNLLTEAHKALFX
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APPLICANT: He Page, Richard WF
APPLICANT: Wells, Jeremy M
APPLICANT: Hanniffy, Sean B
TITLE OF INVENTION: Proteins
FILE REFERENCE: PMC/P2108900
CURRENT APPLICATION NUMBER: US/09/769,736
CURRENT APPLICATION NUMBER: GB 9816335.5
PRIOR APPLICATION NUMBER: GB 9816335.5
PRIOR APPLICATION NUMBER: US/09/169,736
PRIOR APPLICATION NUMBER: US/09/16335.5
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US/0725163
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 212
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SEQ ID NO 18
LENGTH: 822
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Best Local
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TYPE: PRT
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QLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIP 332
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                                                         TPAPGRRKAP - I PDVTPNPGQGHQPDNGGYHPAPPRPNDASQNKHQRDEFKGKTFKELLD
                                                                                                                                                                                                                                       KDAAHADNVRTKEEINRQKQEHSQH-REGG-----TPRNDGAVALARSQGRYTTDDGY 169
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ilarity 29.3%;
Conservative , 9
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; Pred. No. 2.9e-58;
99; Mismatches 236;
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APPLICANT: HAMEL, Jose
APPLICANT: MARTIN, Denis
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 8331-9002
CURRENT APPLICATION NUMBER: US/09/252,088
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: US/60/075,425
EARLIER FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 44
SOSTWARE: PATENTIN Ver. 2.0
SEQ ID NO 15
LENGTH: 793
TYDEN: DEM
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US-09-252-088-15
; Sequence 15, Application US/09252088
; Publication No. US20030031682A1
                                          Query Match
Best Local Similarity
Matches 265; Conserv
                                                                                                                      TYPE: PRT
ORGANISM: group
-09-252-088-15
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      14 ENNRVSYID---GKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYN
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                                          22.3%; Score 927; DB 30.7%; Pred. No. 3.8e tive 115; Mismatches
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                                          DB 11;
3.8e-58;
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Sequence 24, Application US/09769736
Publication No. US20030138775A1
GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Le Page, Richard WF
APPLICANT: Wells, Jeremy M
APPLICANT: Hanniffy, Sean B
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21089W0
CURRENT APPLICATION NUMBER: US/09/769,736
CURRENT FILING DATE: 2003-02-14
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APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Hamel, Josee
APPLICANT: Marcin, Bernard
APPLICANT: Marcin, Denis
APPLICANT: Marcin, Denis
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEG ID NO 369
LENGTH: 906
TYPE: PRT
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PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/125163
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
FINANCE: RESERVE OF SEQ ID NO 24
FINANCE: RESERVE OF SEQ ID NO 24
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US-09-884-465A-369
; Sequence 369, Application US/09884465A
; Publication No. US20030077293A1
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; OTHER INFORMATION:
US-09-884-465A-369
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                                     Best Local Similarity Matches 262; Conserv
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TYPE: PRT
ORGANISM: Streptococcus agalactiae
-09-769-736-24
                                                                                                                                                                    ORGANISM: Artificial Sequence
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 43 GINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVK 102
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                                       Conservative 105;
                                                                                                                                Unknown Organism
                                                    17.4%; Score 723.5; DB 1 27.3%; Pred. No. 2.2e-43;
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Pred. No. 2e-52;
16; Mismatches 103;
                                     Mismatches 290;
                                                                          DB 11;
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                                                              KNKADQDSKPDEDKEHDEVSEPTHPESDEKENHAGLNPSADNLYKPSTDTEETEEEAEDT
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RESULT 24
US-09-884-465A-373
; Sequence 373, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
 APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis

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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptcoccus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 373
LENGTH: 906
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Matches 261
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                    AYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLI
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                                                                              TEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQ
                                                                                                                                                                                                            TLTAKKENVAPRDQEFYDKAYNLLTEA------HKALFXNKGRNSDFQALDKLL
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                                                                                                                                                                                                                                                                       GEGYVFEEKGISRYVFAKD-----LPS-ETVK-----NLESKLSKQESVSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGYVIKVDGKYYVYLKDAAHADNVRTKEEINRQKQEHSQHREGGTPR-----NDGAV 154
AYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLI
                                                             TDDEIQVAKLAGKYTTEDGYIFD----
                                                                                                                     EEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTIELRLPSGEVIKKNLSDFIAGPQITY
                                                                                                                                                  ERLINDESTNIKEKLVD-----SQIEY
                                                                                                                                                                                 --TGTVEN----OPTENKPADSLPEAPNEKPVKPENSTDNGMLNPEGNVGSDPMLDPAL
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Ouellet, Catherine
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APPLICANT: Hamel, Josee
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARR: Patentin version 3.1
SEQ ID NO 371
LENGTH: 906
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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   312 YHFIPYSQ----MSELEERIARI-----IPLRYRSNHWVPDSR-----
                                                                                                                                                                                                                                                 212 LSGRGNLSN--
                                                                                                                                                                                                                                                                                                              194 VVNLLKNSTFNNQNFTLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSGKVF
                                                                                                                                                                                                                                                                                                                                                                           173 ASDIIEDT---GDAYIVPHGD---HYHYIPKNELSAS------ELAAAEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                         146 DGHHADPIDEHKPVGIGHSHSNYELFKPEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 DAAHADNVRTKEEI----NRQKQEHSQHREGGTPRNDGAVALARSQGR--YTTDDGYIFN 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 SSHEQDYPGNAKEMKDLDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIIYPSG----- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 ISEE------LLMKD------PNYKLKDEDIVNEVKGGYVIKVDGKYYVYLK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 GFDANRIIAE-DESGFVMSSGDSNHYFFKKDLTEEQIKAAQKHLEEVKTSHNG---LDSL 92
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                                                             FTVPTSLAYKMASQTIFYPFHAGDTYLRVNPQFAVPKGTDALVRVFDE
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FHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVEVPILEK 400

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; CTHER INFORMATION: US-09-884-465A-333
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                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 333
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 333, Application US/09884465A Publication No. US20030077293A1
                                 Matches
                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                             Query Match
                                                                                                                                                                                                                            APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Shire Biochem, Inc. APPLICANT: Hamel, Josee APPLICANT: Brodeur, Bernard
                                                                                                                         CRGANISM: Artificial Sequence FEATURE:
                                                                                                                                                        TYPE: PRT
                                                                                                                                                                     LENGTH: 900
                                                Local
                               cal Similarity
257; Conserv
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   GINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVK 102
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Martin, Denis
                               Conservative 105; Mismatches 289;
                                                                                                         Unknown Organism
                                             16.2%; Score 675.5; DB 1 26.8%; Pred. No. 6.5e-40;
                                                           DB 11;
                               Indels 309;
                                                          Length
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                                                                                                          US-09-252-088-16
                                                           Sequence 16, Application US/09252088 Publication No. US20030031682A1 GENERAL INFORMATION:
APPLICANT: BRODEUR, Bernard R. APPLICANT: RIOUX, Clment APPLICANT: BOYER, Martine APPLICANT: CHARLEBOIS, Isabelle
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155 ALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAA----EA
TDEAEI----PGTPSIRQNAMETLTGLKSSLLLGTKDNNTISAEVDSLLALLKESQPAPI 899
                                              --EAEVILAKVTDSSLKANATETLAGIRNNITLQIMDNNSIMAEAEKILALIKGSNPSSV 790
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                                                                                                                                                                            LGKKDHSEDPNKNFKADE--EPVEETPAEPE------VPQVETEKVEAQLK--
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                                                                                                                                                                                                                                                                                             IPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHV-
                                                                                                                                                                                                                                                                                                                                                              AYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLI
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                                                                                                                                                                                                                                            -NIKFEWFDEGLYEAPKGYSLEDLLATVKYYVE-----PR---
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CURRENT APPLICATION NUMBER: US/09/252,088
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: US/60/075,425
EARLIER FILING DATE: 1998-02-20
INVMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 715
TYPE: PAT
ORGANISM: group B streptococcus
US-09-252-088-16
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Best Local Similarity
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APPLICANT: MARTIN, Denis
TITLE OF INVENTION: NOVEL GROUP B STREPTOCCCCUS
FILE REFERENCE: 8331-9002
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                                                                                            EKVEAQLKEAEVILAKVTDSSLKANATETLAGIRNNLTLQIMDNNSIMAEAEKILAILKG
                                                                                                                                            QIIHSAEEVQKALAEGRFATPDGYIFDPRDVLAKETFVWKDGSFSIPRADGSSLRTINKS
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    SNPSSVSKEK 794
                                                DLSQAEWQQAQELLAKKN----TGDATDT--
                                                                                                                                                                                                                                                                                  YKAPNGYTLEDLFATIKYYVEHPDERPHSNDGW------GNASEHVLGKKDHSEDPNK
                                                                                                                                                                                                                                                                                                                                                                                                                            --FAEQELM-
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                                                                                                                                                                                                                                    -TRDQIATVKYVMQHPEVRP---DVWSKPGHEESGSVIPNVTPLDKRAGMPNW 538
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SEQ ID NO 370
LENGTH: 906
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                       RESULT 29
US-09-884-465A-372
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US-09-884-465A-370
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                                                                                                                                     Sequence 372, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
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                                                                        APPLICANT:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
                          APPLICANT:
TITLE OF I
                                                                                            APPLICANT:
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
    REFERENCE:
ANT: Brodeur, Bernard
ANT: Martin, Denis
ANT: Charland, Nathalie
ANT: Ouellet, Catherine
DF INVENTION: Streptococcus A
SFERENCE: 055190-0044
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Martin, Denis
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45.6%; Pred. No. 1e-37;
tive 40; Mismatches 74;
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APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044

CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-66-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 258
LENGTH: 272
TYPE: PRT
CRGANISM: Artificial Sequence
FEATURE:
COURSE THEORYMAND.
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CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 372
LENGTH: 906
TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 258, Application US/09884465A Publication No. US20030077293A1
Query Match 15.4%; Score 643; DB 11; Best Local Similarity 46.1%; Pred. No. 2.3e-38; Matches 140; Conservative 39; Mismatches 71;
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
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US-09-884-465A-344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
SEQ ID NO 344
LENGTH: 895
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Best Local :
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APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
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                                                        687 EHV-LGKKDHSEDPNKNFKADE--EPVEETPAEPE-------VPQVETEKVEAQ 730
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                    DHVRKNKADQDSKPDEDKEHDEVSEPTHPESDEKENHAGLNPSADNLYKPSTDTEETEEE
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Pred. No. 1.4e-37;
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Length 895; Indels

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RESULT 33
US-09-884-465A-300
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                                              Sequence 300, Application US/09884465A Publication No. US20030077293A1 GENERAL INFORMATION:
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SEQ ID NO 343
LENGTH: 901
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Best Local Similarity
Matches 140; Conserv
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-66-20
PRIOR FILING DATE: 2000-66-20
NUMBER OF SEC IN NOC. 200
                APPLICANT: Shire Biochem, Inc. APPLICANT: Hamel, Josee
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NUMBER OF SEQ ID NOS: 384
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ORGANISM: Artificial Sequence
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Martin, Denis
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; Pred. No. 1.4e-37;
39; Mismatches 71;
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                                                                            PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 301
LENGTH: 272
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SEQ ID NO 300
LENGTH: 272
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TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-004
CURRENT FILLING DATE: 2001-06-20
CURRENT APPLICATION NUMBER: 60/212,683
PRIOR APPLICATION NUMBER: 60/212,683
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                                                              LENGTH: 2'
TYPE: PRT
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FEATURE:
OTHER INFORMATION: Unknown Organism
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Martin, Denis
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Ouellet, Catherine
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o. US20030077293A1
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Pred. No. 3.2e-38;
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US-09-884-465A-336
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Matches 140
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SEQ ID NO 336
LENGTH: 894
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
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APPLICANT: Hamel, Josee
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 GSLIIPSYDHYHNIKFEWFDEGLYEAPKGYSLEDLLATVKYYVE-----PR-----NAS
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Martin, Denis
                                                                                                                                                                                Conservative
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46.1%; Pred. No. 3.2e-38;
Live 39; Mismatches 71
                                                                                                                                                                                           15.3%; Score 636; DB 11; 45.3%; Pred. No. 4.5e-37;
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                                                                                                                                                                                                          Length 894;
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RESULT 37
US-09-884-465A-332
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APPLICANT: Hamel, Josee
APPLICANT: Brodeeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                               731
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 Application US/09884465A
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US-09-884-465A-335
; Sequence 335, Application US/09884465A
; Publication No. US20030077293A1
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CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEO ID NOS: 384
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 335
LENGTH: 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.3%; Score 636; DB 11; Best Local Similarity 45.3%; Pred. No. 4.6e-37; Matches 140; Conservative 40; Mismatches 75;
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
                                                                                                                                                                                                                                                                                    627 GNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNAS 686
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AEDTTDEÄEI----PGTPSIRQNÄMETLTGLKSSLLLGTKDNNTISAEVDSLLALLKESQ
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                          APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 051190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARPE: Datation version 3 1
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 332
LENGTH: 906
Type: nom
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SOFTWARE: PatentIn
SEQ ID NO 293
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
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Martin, Denis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.3%; Score 636; DB 11;
45.3%; Pred. No. 4.6e-37;
40. Mismatches 75;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 294
LENGTH: 272
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Best Local Similarity
Matches 139; Conserv
                                                                                                                    Matches
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                                                                                                                               Query Match
Best Local Similarity
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APPLICANT:
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CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
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                                                                                                                                                                                                                                                TYPE: PRT
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567 VAAQAYTKEKGILPESPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKN
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Pred. No. 1e-37;
9; Mismatches 72;
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SEQ ID NO 295
SEQ IT NO 272
TYPE: PRT
ORGANISM: Artificial Sequence
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PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARD THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE PRIOR SERVING THE 
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CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
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Dublication No. US2003007729;
GENERAL INFORMATION:
APPLICANT: Shire Biochem, I
APPLICANT: Hamel, Josee
APPLICANT: Marcian, Bernar
APPLICANT: Martin, Denis
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APPLICANT: Owellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
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US-09-884-465A-340
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NUMBER OF SEQ ID NOS: 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Unknown Organism
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268
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PAPIQGPQI 276
                                                                                  AEDTTDEAEI ---- PGTPSIRQNAMETLTGLKSSLLLGTKDNNTISAEVDSLLALLKESQ
                                                                                                                            LK----EAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSN 786
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                                       PSSVSKEKI 795
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45.0%; Pred. No. 2e-36;
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42

151 989

211

APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20

US-09-884-465A-342; Sequence 342, Application US/09884465A; Publication No. US20030077293A1

GENERAL INFORMATION:

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RESULT 43
US-09-884-465A-339
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APPLICANT: Martin, Denis
APPLICANT: Martind, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptcoccus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
                                                                                                        US-09-884-465A-339
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PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 342
LENGTH: 894
                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 339
LENGTH: 900
                                                Query Match
Best Local Similarity
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Best Local Similarity
                                  Matches 139;
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                                                                                                                                                                        LENGTH: 90
TYPE: PRT
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ORGANISM: Artificial Sequence
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507 QIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEK 566
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                                              Score 627; DB 1
Pred. No. 2e-36;
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Pred. No. 2e-36;
0; Mismatches 76;
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US-09-884-465A-341
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
SEQ ID NO 341
LENGTH: 900
TYPE: PRT
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APPLICANT: Shire Biochem,
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Unknown Organism
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                                                                                                                                                                                                                                                                                                                                     Local Similarity
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LK----EAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSN 786
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Brodeur, Berrin, Denis
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                                                 DHVRKNKADQDSKPDEDKEHDEVSEPTHPESDEKENHAGLNPSADNLYKPSTDTEETEEE
                                                                                                                                                  GNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNAS
                                                                                                                                                                                    AAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYTVEVKN
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                                                                                  EHV-LGKKDHSEDPNKNFKADE--EPVEETPAEPE-----
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45.0%;
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Pred. No. 2e-36;
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Length 272; Indels

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RESULT 46
US-09-884-465A-296
; Secuence 296, Application US/09884465A
; Publication US20030077293A1
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                                          GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
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SOFTWARE: Patentin version 3.1
SEQ ID NO 302
LENGTH: 270
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Best Local
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
        APPLICANT:
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Brodeur, Bernard
Martin, Denis
Charland, Nathalie
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Martin, Denis
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                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 298
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Best Local Similarity
Matches 138; Conserv
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CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 296
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
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                                            OTHER INFORMATION: Unknown Organism
                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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ilarity 45.4%;
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Pred. No. 4.6e-37;
9; Mismatches 73;
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APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 05519-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 299
LENGTH: 272
TYPE: PRT
ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Unknown Organism
US-09-884-465A-299
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US-09-884-465A-299
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Best Local Similarity
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Publication No. US20030077293A1
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                                                                                          AAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYTVEVKN 102
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   EHV-LGKKDHSEDPNKNFKADE--EPVEETPAEPE---
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Martin, Denis
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Pred. No. 4.6e-37;
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9; Mismatches
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   -VPQVETEKVEAQ 730
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RESULT 50
US-09-884-465A-345
; Sequence 345, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 346
LENGTH: 895
TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-004
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILLING DATE: 2001-06-20
CURRENT FILLING DATE: 60/212,683
PRIOR APPLICATION NUMBER: 60/212,683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                          567 VAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKN
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AEDTTDEAEI----PGTPSIRQNAMETLTGLKSSLLLGTKDNNTISAEVDSLLALLKESQ
                                                     LK----EAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSN 786
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Martin, Denis
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APPLICANT: Brodeur, Bernard
APPLICANT: Brodeur, Bernard
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
FILE REFERENCE: 055190-0044
CURRENT APPLICATION: Streptcoccus Antigens
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
INUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 345
LENGTH: 901
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Unknown Organism
US-09-884-465A-345
Search completed: November 14, 2003, 10:50:45 Job time : 343 secs
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APPLICANT: Hamel, Josee
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Perfect score:
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SUMMARIES

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AR120265 Sequence 55 from AR120265 AR120265		199	98 20 0.8	196 20 0.8	194 20 0.8	193 20 0.8	191 20 0.8 192 20 0.8	190 20 0.8	9 20 0.8	7 20 0.8	186 20 0.8	185 20 0.8	183 20 0.8	182 20 0.8	181 20 0.8	179 20 0.8	178 20 0.8	176 20 0.8	175 20 0.8	173 20 0.8	172 20 0.8	171 20 0.8	169 20 0.8	168 20 0.8	166 20 0.8	165 20 0.8	163 20 0.8	162 20 0.8	160 20 0.8	159 20 0.8	157 20 0.8	156 20 0.8	155 20 0.8	153 20 0.8	52 20 0.8	50 20 0.8	149 20 0.8	148 20 0.8	146 20 0.8	145 20 0.8	44 20 0.8	20 0.8	41 20 0.8	139 20 0.8
AR120265 Sequence 55 AR120265	ALIGNMENTS	199 20 0.8 200 20 0.8	98 20 0.8 203223 2 98 20 0.8 204082 9	196 20 0.8 200602 10 AL59099	194 20 0.8 199050 1 195 20 0.8 200602 10	193 20 0.8 197658 2 AL646094	191 20 0.8 196491 9 192 20 0.8 197658 2	190 20 0.8 196107 8	9 20 0.8 194907 2	7 20 0.8 194425 5 8 20 0.8 194785 3	186 20 0.8 193301 9	185 20 0.8 193057 9	183 20 0.8 192129 2	182 20 0.8 192096 2	181 20 0.8 191553 2	179 20 0.8 189350 2	178 20 0.8 186165 9	176 20 0.8 182658 2 177 20 0.8 185845 9	175 20 0.8 182632 9	173 20 0.8 181584 2 174 20 0.8 182446 2	172 20 0.8 180571 9	171 20 0.8 180450 3	169 20 0.8 177071 2	168 20 0.8 175838 2	166 20 0.8 171370 9	165 20 0.8 171115 9	163 20 0.8 168842 5	162 20 0.8 166226 9	160 20 0.8 161311 2	159 20 0.8 161279 2	157 20 0.8 157812 2	156 20 0.8 156724 2	154 20 0.8 152806 2	153 20 0.8 150192 2	52 20 0.8 148592 2	50 20 0.8 144722 9 51 20 0.8 147829 2	149 20 0.8 137586 9	148 20 0.8 137519 8	146 20 0.8 133418 9	145 20 0.8 131316 2	44 20 0.8 127313 2	.42 20 0.8 110590 2 BX001021	41 20 0.8 110000 2	139 20 0.8 106689 9 AC008919
2389 bp 55 from patent US 6159469. .1 GI:14103841	ALIGNMENTS	199 20 0.8 205667 2 200 20 0.8 206624 9	97 20 0.8 203223 2 AC127395 98 20 0.8 204082 9 AC005323	196 20 0.8 200602 10 AL590997	194 20 0.8 199050 1 SAG766850 195 20 0.8 200602 10 AL590997	193 20 0.8 197658 2 AL646094	.191 20 0.8 196491 9 AC092832 .192 20 0.8 197658 2 AL646094	190 20 0.8 196107 8 ATCHRIV34	9 20 0.8 194907 2 AC129616	7 20 0.8 194425 5 AL807818	186 20 0.8 193301 9 CNS01DRJ	185 20 0.8 193057 9 ACC22441	183 20 0.8 192129 2 AC134667	182 20 0.8 192096 2 AC126838	181 20 0.8 191553 2 AL772233	179 20 0.8 189350 2 AC136628	178 20 0.8 186165 9 AC112187	176 20 0.8 182658 2 AC084743	175 20 0.8 182632 9 AC007282	173 20 0.8 181584 2 AC017027	172 20 0.8 180571 9 AC113425	171 20 0.8 180450 3 AE014835	169 20 0.8 177071 2 AC128090	168 20 0.8 175838 2 AC116356	166 20 0.8 171370 9 AC004021	165 20 0.8 171115 9 AC068385	163 20 0.8 168842 5 AL929548	162 20 0.8 166226 9 AC022308	160 20 0.8 161311 2 AC137012	159 20 0.8 161279 2 AC125902	157 20 0.8 157812 2 AC055805	156 20 0.8 156724 2 AC016306	155 20 0.8 152806 2 AC129725	153 20 0.8 150192 2 AC122555	52 20 0.8 148592 2 AC125190	50 20 0.8 144722 9 AC008831	149 20 0.8 137586 9 AC106775	148 20 0.8 137519 8 ATT1P17	146 20 0.8 133418 9 AL353709	145 20 0.8 131316 2 AC031985	.44 20 0.8 127313 2 AC078977	.42 20 0.8 110590 2 BX001021 BX00	.41 20 0.8 110000 2 PEMAL/P1_03 Cont	139 20 0.8 106689 9 AC008919 AC00

Qy	Qy dd	Qy Db	D Qy	Qy Db	Qу	Qy db	d dd	Qy Db	Qy Db	Qy db	Qy Db	Qy Db	Qy Db	Query Mai Best Loca Matches	BASE COUNT	TITLE JOURNAL FEATURES	REFERENCE AUTHORS	KEYWORDS SOURCE ORGANISM
781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840	721 TGTAAGCAATCCAGGAACTACAAATACTAACAAGAAGAACAACAAGAACACTAACAGTCA 780	661 TTCANGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720	601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660	541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600	481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540	421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480	361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC	301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360 	241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGGATATTGTTAATGA 300	181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240	121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180	61 TATAGATGGAAAACAAGCGAAGCGAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120	1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60	Match 100.0%; Score 2389; DB 6; Length 2389; ocal Similarity 100.0%; Pred. No. 0; s 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ce 1 2389 /organism="unknown" T 830 a 461 c 486 g 611 t 1 others	Fannon, M.R. and Rosen, C.A. Streptococcus pneumoniae antigens and vaccines Patent: US 6159469-A 55 12-DEC-2000; Location/Qualifiers	<pre>Unclassified. 1 (bases 1 to 2389) Choi,G.H., Kunsch,C.A., Barash,S.C., Dillon,P.J., Dougherty,B.,</pre>	Unknown. M Unknown.
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g dy	d 4d	p &	S B &	P &	₽ ₹	S & &	Db Qy	D 49	S B &	, B &	S & &	₽ \ \$	S & &	Db Q	D Q	B Q	Db .	OV Db
1861 TACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAATAT 1920 	01 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1 01 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1	1 TOCATOTIC CASACUCASA INTERCENTAL CONSTITUTION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSION IN INCLUSIONI IN INCLUSIONI IN INCLUSIONI IN INCLUSIONI IN INCLUSIONI IN INCLUSIONI IN INCLUSIONI IN INCLUSIONI IN INCLUSIONI IN INCLUSIONI IN INCLUSIONI IN INCLUSIONI IN INCLUSI	BI CCITICIGAL AAGGAMAAGITIGCAGCICAAGCCTATACTAAAGAAAAAAGGTATCCTACC 1 BI CCTTTTCTGATAAGGAAAAAGTTGCAGCCTCAAGCCTATACTAAAGAAAAAAGGTATCCTACC 1 AT TOOLTCTGATAAGGAAAAAGTTGCAGCCTCAAGCCTATACTAAAGAAAAAAGGTATCCTACC 1	21 TGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATGGA	61 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 61 AGCTGATAAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1	01 ACTTGGCAAACCAAATTCTCAAATTGAGTATAGAGTATAGAGAGAG	41 TAAAGAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1 	BI TAATICTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA	TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 	bl TGTTTCACACACTTTAACTGCTAAAAAAAGAAATGTTGCTCCTCGTGACCAAGAATTTTA 1 61 TGTTTCACACACTTTAACTGCTAAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1	201 GAANGATTTACCATICTGAAACTGTTAAAAAATCTTGAAAGCAGGTTATCAAAACAACAKGAGAGTTATCAAAACAACAKGAGAGTTATCAAAACAACAKGAGAGAGAGAGAAAATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAGAG	41 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAGGGCATCTCTCGTTATGTCTTTGC 41 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC	81 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTTGGTTAGTCAGCTGGT 1 81 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 1 81 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 1	021 GGTACCAGATTCAAGGCCAGAACAACTCCACAACTGCTCCGGAACCTAGTCCAGG 021 HIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	61	901 AGCTAGAGGTGTTGCAGTGCCACAGGGAGATCATTACCACTCCATCCCTTACTCTCAAAT 960 		781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840

Query Match Best Local Similarity 100.0%; Score 2389; DB 6; Length 2389; Best Local Similarity 100.0%; Pred. No. 0; Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 2389; TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60	PC G01N33/68 CC Strandedness: Double; CC Topology: Linear; CC Topology: Linear; FEATURES FOURTES Location/Qualifiers Location/Qualifiers 1.2389 /01289 /02931388888888888888888888888888888888888	REFERENCE 1 (Bases 1 to 2389) AUTHORS Kunsch, C.A., Choi, G.H., Johnson, S.L. and Hromockyj, A. TITLE Streptococcus pneumoniae antigens and vaccines JOURNAL HUMAN GENOME SCIENCES INC COMMENT PN JP 2001505415-A/28 PD 24-APR-2001 PF 30-OCT-1997 JP 1998520667 PR 31-OCT-1996 US 60/029960 PI CHARLES A KUNSCH, GIL H CHOI, SYDNOR L JOHNSON, ALEX HROMOCKYJ PC G1N13/31, G12N5/18, G12N1/21, C07K14/315, C12Q1/68, A61K39/09, PC G01N33/569,	RESULT 2 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 CESSION BD063274 CESSION BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 CESSION BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD063274 BD0632	Db 2221 AGTAACGGATTCTAAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA 2280 Qy 2281 TTTGACTCTTCAAATTATTGGATAACAATAGTATCATGGCAGAAGCAGAAAATTACTTGC 2340 Db 2281 TTTGACTCTTCAAATTATTGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC 2340 Db 2281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC 2340 Qy 2341 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAAGAAAAAAAA	2101 2161 2161 2161 2221	1921 TAAATTTGCTTTGATGATGATCACACATACAAAGCTCCAAATGGCTATACCTTTGAAGA 1981 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGACGTCCACATTCTAATGA	OY 1921 TAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGGAAGA 1980
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021 GGTACCAGATTCAAGGCCAGAACCAACTCCACAACCGAACCCAGTCCAGG 1080 021 GGTACCAGHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	B41 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCACCACAAATCACAAGTCGAAAC 900 B41 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCACCACTACAAATCACAAGTCGAAAC 900 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCCCAAAT 960 901 AGCTAGAGTGTTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCCCAAAT 960 961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020 961 GTCTGAATTGGAAGAACGAATCGCTCGTTATTATCCCCTTCGTTATCGTTCAAACCATTG 1020		481 AGACGCIATACIACAGATGATGATTATACCITTAATGCITCIGATACATACAATAGAATGAGTT 600 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600 541 TGGTGATGCTTATATCGTTCCTCATGGAGAAGCCTTCCTATCTGGTCGAGAAATCTGTCAAA 660 601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660 601 ATCAGCTAGCGAGTTGGCTGCAGAAATAGGGATAGAAGTAGGAGAAATCTGTCAAA 660 601 ATCAGCTAGCGAGTTGGCTGCAGAAATTAGGGATAGAAATCTGGTCGAGGAAATCTGTCAAA 660	361 TGCCCACGCGGATAACGTCCGTACAAAGAGGAAATCAATC	241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300	61 TATAGATGGAAAACAAGCGACGAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120	TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60

	161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCCAACTCAAAGAAGCAGAAGTTTTGCCTTGCC	
2220	2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGC	
2160 2160	<u> </u>	
2100 2100	041 TGGATGGGGCAATGCCAGTGAGCATGTGTTAGG 	
2040	981 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAA 	
1980 1980	921 TAAATTTGCTTGGTTTGATGATCA(
1920 1920	TACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCT	
1860 1860	801 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAC	
1800	741 TCCATCTCCAGAC	
1740 1740	681 CCTTTCTGATAAGGAAAAAGTTGCAG 681 CCTTTCTGATAAGGAAAAAGTTGCAG	
1680 1680	621 TGAAGGAGATGCATATGTAACGCCTC	
1620 1620	61 AGCTGATAAG	
سر ب	01 ACTTGGCAAACCAAATTCTCAAATTGAG	
1500 1500	441 TAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGC	
	81 TAATTCTGATTTC	
1380 1380	321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGG	
1320 1320	261 TGTTTCACACACTTTAACTGCTAAAAAAGA 	
1260 1260	N N	
1200 1200	1 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCG	
1140	1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT	

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BASE COUNT	CDS	gene		Bource	TITLE JOURNAL	REFERENCE AUTHORS	JOURNAL MEDLINE PUBMED	TITLE	REFERENCE AUTHORS	SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	RESULT 3 AF291695 LOCUS DBFINITION	Оу 23 Db 23	Db 22	Qy 22	Qy 22
/note="PhtA" /codon start=1 /trans[table=11 /trans[table=1] /trans[table=1] /product="pneumococcal histidine triad A protein" /protein id="AAR1915,1" /db_xref="G1:13345013" /translation="MKINKKYLVGSAAALILSVCSYELGLYQARTVKENNRVSYIDGK QATQKTENLTPDEVSKREGINAGQIVIKITDQGYVTSHGGHYHYYNQKVPYDAIISEE LLMKDENYKLKDEDIVMEVKGGYVIKVDGKYYVYLKDAAHADNVRTKEEINRQKQEHS QHREGGTPRNDGAVALARSQGRYTTDDDGY_ENASDIIEDTGDAYIVTHGEHYYIYSNUSN TNSQASQSNDIDSLLKQLYKLPLSQHHVESDGLYUPDPAQITSRTARGVAVPHGDHYHF IPYSQMSELEBRIARIPLAKSKORTYRRQNSDNITSRTNWVPSVSNPGTININTSNNSN TNSQASQSNDIDSLLKQLYKLPLSQHHVESDGLYUPDPAQITSRTARGVAVPHGDHYHF IPYSQMSELEBRIARIPLAKSTSNIWTVPDSRPEQSEPOPPEPSPGPOPAPNLKIDSN SSLVSQLVKKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQDSVSHTLTAKKE NVAPRDQEFYNKAYNLLTEAHKALFXNKGRNSDFOALDKLLERLNDESTNKEKLUDL LAFLAPIITHPERLGKPNSQIEYTEDEVRIAQKLADKYTTSDGYIFDENDIISDEGDAYV TPHMGHSHMIGKOSLSDKEKVAAQAYTKEKGILPBSPDAUVXANFTGDSAAAIYNRVK GEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYNIKFAWEDDHTYKAPNGYTLEDLF ATIKYYVEHPDERPHNDGWGNASEHVLGKCHSSEDVKNIFKADEEVEETPAEPEVP QVETTEKVEAQLKEARVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKL LALLKGSNPSSVSKEKIN" 888 a 476 c 516 g 660 t 1 others	/ 3cm / 254 / 1 91254 / /qene="phtA"	91. 2541 91. (2541 Gene-Whith	/organism= orreproductors premindings /mol_type="genomic DNA" /strain="NA" /sh yref="rayon.1313"		Direct Submission Submitted (01-AUG-2000) Molecular Biology, Human Genome Sciences, Inc., 9410 Key West Ave., Rockville, MD 20850, USA	2 (bases 1 to 2541) Choi,G.H.	Intect. Immun. 69 (3), 1593-1598 (2001) 21116976 11179332	Use of a whole genome approach to identify vaccine molecules affording protection against Streptococcus pneumoniae infection	1 (bases 1 to 2541) Wizemann,T.M., Heinrichs,J.H., Adamou,J.E., Erwin,A.L., Kunsch,C., Choi,G.H., Barash,S.C., Rosen,C.A., Masure,H.R., Tuomanen,E., Gayle,A., Brewah,Y.A., Walsh,W., Barren,P., Lathigra,R., Hanson,M., Lancermann S. Johnson S. and Koenig S.		AF291695.1 GI:13345012	AF291695 2541 bp DNA linear BCT 15-MAR-2001 Streptococcus pneumoniae pneumococcal histidine triad A protein (phtA) gene, complete cds.	2341 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAAATAAAC 2389 	2281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC 2340	2281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC 2340	2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA 2280

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181 TTCACATGGCGACCACTATCATTACAATGGTAAGGTTCCTTATGACGCTATCAG	Qy 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60	source 1. 2406 /organism="Streptococcus pneumoniae" /mol_type="genomic DNA" /db_xref="taxon:1313" BASE COUNT 834 a 461 c 490 g 621 t ORIGIN Query Match 97.9%; Score 2338; DB 6; Length 2406; Best Local Similarity 100.0%; Pred. No. 0; Matches 2388; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	SOURCE Streptococcus pneumoniae ORGANISM Streptococcus pneumoniae Bacteria, Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus. REFERENCE 1 TITLE Streptococcus pneumoniae proteins and nucleic acids JOURNAL Patent: WO 0.0077021-A 2347 03-OCT-2002; Chiron Spa (IT); THE INSTITUTE FOR GENOMIC RESEARCH (US) FEATURES Location/Qualifiers	RESULT 4 AX569139 LOCUS AX569139 DEFINITION Sequence 2347 from Patent WO02077021. ACCESSION AX569139 VERSION AX569139 VERSION AX569139.1 GI:26002636 KEYWORDS	Qy 2341 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGGAAAAAATAAAC 2389 [2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA 228	Qy 2101 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC 2160
Qy 1261 TGTTTCACACACTTTAACTGCTAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320	Db 1098 CCCGCAACCTGCACAATCTTAAAAATCTTGAAAAGGCAAGTTATCAAAACAAGAGAG 1277	918 AGCTAGÁAGTGTTGCAAGTGCCÁCAGGÁAGÁTCATTATCCCTTTATCCCTTAÁCTCTCAÁAGT 961 GTCTGAATTGGAAGAACGAATCGCTGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 978 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 978 GTCTGAATTGCAAGGACAACCAAGTCCACAACCGAACCTAGTCCAGGCCAGG 1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGAACCTAGTCCAGGCCAGG 1038 GGTACCAGATTCAAGGCCAGAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGGG 1038 GGTACCAGATTCAAGGCCAGAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG	Oy 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840	Oy 661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAGACCTGGGTACCTTC 720	OD 558 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 617 QY 601 ATCAGCTAGCGAGTTGGCTGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660	481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 5	Qy 361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCGACAAAAACAAGAGCATAG 420

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1 (bases 1 to 8195)

Kunsch,C.A., Choi,G.H., Dillon,P.S., Rose Fannon,M.R. and Dougherty,B.A.
Streptococcus pneumoniae polymucleotides
Patent: US 6420135-A 94 16-JUL-2002;
Location/Qualifiers
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                                                                             TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA
                                                                                                                       TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC
                                                                                                                                                                  ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA
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 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900
                                                                  TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA
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Ouerv Match	1921 TAAATTTGCTTGGTTTGATGATCACACATAGAAAGGTCCAAATGGCTATACCTTGGAAGA 1980
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FEATURES SOURCE	1801 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1860
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PR PI Si	1621 TGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG 1680
COMMENT OS PN PD	1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1620
	1501 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGGTCGTATTGCTCAATT 1560
ORGANISM univ	1441 TAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1500
ACCESSION BDO VERSION BDO KEYWORDS JP	1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGAA
t to	1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380
Db 5393 G	1261 TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320
5333	1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 1260
5273	1141 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC 1200
5213	1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 1140
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Kunsch, C.A., Choi, G.H., Dillon, P.J., Rosen, C.A., Bara, S.C.,

Fannon, M. and Dougherty, B.A.

Polynuclectide of Streptcocccus pneumoniae and sequence

Patent: JP 2001501833-A 94 13-FEB-2001;

HUMAN GENOME SCIENCES INC

OS Unidentified

PN JP 200150183-A/94

PD 13-FEB-2001

PF 30-CCT-1996 US 60/029960

PR 31-CCT-1996 US 60/029960

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PR 31-CCT-1996 US 60/029960

PR CHARLES A KUNSCH, GIL H CHOI, PATRICK J DILLON, CRAIG A ROSEN, PI
                                                                                                                                                                                                                                                                                        STEVEN C BARASH,
MICHAEL FANNON, BRIAN A DOUGHERTY
CI2N15/09, A01K67/027, C07K14/315, C07K16/12, C12N1/15, C12N1/19,
C12N1/21,
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et e	Peterson, S Durkin, A. S Durkin, A. S Umayam, L. A. S Khouri H. , Feldblyum, Loftus, B. J. Dougherty, Direct Sub Submitted Medical Cc Medical Ci	Peterson, S., Heidelberg, J., DeBoy, R.T., Haft, D.H., Dedoon, R.J., Burkin, A.S., Gwinn, M., Kolonay, J.F., Nelson, W.C., Peterson, J.D., Umayam, L.A., White, O., Salaberg, S.L., Lewis, M.R., Radune, D., Holtzapple, E., Khouri, H., Wolf, A.M., Utterback, T.R., Hansen, C.L., McDonald, L.A., Feldblyum, T.V., Angiuoli, S., Dickinson, T., Hickey, E.K., Holt, I.E., Lottus, B.J., Yang, F., Smith, H.O., Venter, J.C., Dougherty, B.A., Morrison, D.A., Hollingshead, S.K. and Fraser, C.M. Complete genome sequence of a virulent isolate of Streptococcus pneumoniae Science 293 (5529), 498-506 (2001) 21557209 11463916 2 (bases 1 to 10256) Tettelin, H., Nelson, K.E., Paulsen, I.T., Eisen, J.A., Read, T.D., Poterson, R., Nelson, K.E., Paulsen, I.T., Eisen, J.A., Read, T.D.,	AE007418 Streptococcus pneumoniae TIGR4 section genome. AE007418 AE005672 AE007418.1 GI:14972649 Streptococcus pneumoniae TIGR4 Streptococcus pneumoniae TIGR4 Bacteria; Firmicutes; Lactobacillales; Streptococcus. 1 (bases 1 to 10256)	2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGC
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  TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320
                                                                               GAAAGATTTACCATCTGAAAACTGTTAAAAAATCTTGAAAAGCAAGTTATCAAAAACAAGAGAG 1260
                                                                                                                                         ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC
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/note="seq 4979 too long: 2.162.598 bases~replaced by
/note="seq 4979 too long: 2.162.598 bases~replaced by
following seq:~seq 4979: from 0.000.001 to 0.349.980-seq
4980: from 0.300.001 to 0.649.980-seq 4981: from 0.600.001
to 0.949.980~seq 4982: from 0.900.001 to 1.249.980-seq
4983: from 1.200.001 to 1.549.980-seq 4984: from 1.500.001
to 1.849.980-seq 4985: from 1.800.001 to 2.149.980~seq
4986: from 2.100.001 to 2.162.598"
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LeBlanc, D.J., Lee, L McAhren, S., McHenne, Norris, F.H., O'Gara	1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1620 	용 &
REFERENCE 1 (bases 1 to 1032) AUTHORS Hoskins, J. A., Alborn DeHoff, B. S., Estrem	1501 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT 1560 	유왕
SOURCE Streptococcus pneum SOURCE Streptococcus pneum ORGANISM Streptococcus pneum Bacteria; Firmicute	1441 TAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1500	당 왕
ACCESSION AE008479 AE007317 VERSION AE008479.1 GI:1545 KEYWORDS	1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATGA	. B. 8
RESULT 9 AE008479/c AE008479 LOCUS DETINITION Streetscoories means	1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380	g Q
Db 104610 GTTGTTAAAAGGAAGTA	1261 TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320 	d dq
104670	1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 1260 	d do
104730 AGTAACGGATTCTAGT	1141 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC 1200	8 A
104790	1081 CCGGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTTCT	D Qy
104850	1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080	d dd
104910	961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020 	9g 9g
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1.05030	841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900	B Q
90	781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840 	B 8
105150	721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780 	B 8
105210	661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAACTGGGTACCTTC 720 	d dd
105270	601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660	Qy dd
105330	541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600	유 성
Qy 1621 TGAAGGAGATGCATATG		

2341 104610	2281 104670	2221 104730	2161 104790	2101 104850	2041 104910	1981 104970	1921 105030	1861 105090	1801 105150	1741 105210	1681 105270	1621 105330
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	2340 104611	2280 104671	2220 104731	2160 104791	2100 104851	2040 104911	1980 104971	1920 105031	1860 105091	1800	1740 105211	1680 105271

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Streptococcus pneumoniae R6 section 95 of 184 of the complete
genome.
GCESSION
AE008479.1 GI:15458677
SYWORDS
SURCE
ORGANISM
Streptococcus pneumoniae R6
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus
1 (bases 1 to 10320)
AUTHORS
DeHoff, B.S., Estrem, S., Fritz, L., Fu, D.-J., Fuller, W., Geringer, C.,
Gilmour, R., Glass, J.S., Khoja, H., Kraft, A., LaGace, R.,
LeBlanc, D.J., Lee, L.N., Lefkowitz, E.J., Lu, J., Matsushima, P.,
Norris, F.H., O'Gara, M., Peery, R., Robertson, G.T., Rockey, P.,
Sun, P.-M., Winkler, M.E., Yang, Y., Young-Bellido, M., Zhao, G.,

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PUBMED
REFERENCE
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JOURNAL
MEDLINE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome of the bacterium Streptococcus pneumoniae strain R6 J. Bacteriol. 183 (19), 5709-5717 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt Zook,C.} , {\tt Baltz,R.H.}, {\tt Jaskunas,S.R.}, {\tt Rosteck,P.R.\ Jr.}, {\tt Skatrud,P.L.} and {\tt Glass,J.I.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
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                                                                                          complement (2151.
/gene="spr1059"
complement (2151.
/gene="spr1059"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / tränslation="MTTKXANITIEXIEMSEVDFNBAVNYEFFSDTCQLANSIYQSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (1923. .2081)
/gene="spr1058"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (1923. .2081)
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transl_table=
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Gace, R.,
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                                                                                                                                                                                                                                                                                                                              PVEETPAEPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIM
DNNSIMAEAEKLLALLKGSNPSSVSKEKIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLYEAPKGYSLEDLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIGHYHYI PKNELSASELAAAKAFILSGRGNLSNSRTYRRQNSDNTSRTIMWVPSYSNPG
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QPAPNPQÞAPSNÞIDEKLVKEAVRKVGDGYVFEENGVPRYI ÞAKDLSAETAAGIDSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_unit=Rup_A
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complement(2725.
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                                                                                                                                                                                  gene="pts1"
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ACTTGCAAGCCAAATTCTCAAATTGAGTATACTGAAGAAAAAAAA	6488 TAATACCAAAATTCTCAAATTGAGGATACTGAAGACGAAGTTCGTATACCCAGAGGGTCG 630 1381 TAATTCTGATTTCCAAGCCTTAGACAATTATTAGAAGCCCTTGATTGA	Db 6668 ACGARAGTTGGGGARAGTTTAAATGTATTGAAAAGGAAAGG	6848 GICTGAATTGAAGCGAATCGCTCGTATTATTCCCTTCGTTATCGTTCAAACCATTG- 1021 GGTACCAATTCAAGGCCAGAACCACCACCACCGACTCCGGAACCTAGTCCAGG- 1021 GGTACCAGATTCAAGGCCAGAACCAAGTCCACCACCGACTCCGGAACCTAGTCCAGG- 11	Db 7028 AGCAAGTCAAAGTANTGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 6969 Qy 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGGACAAATCACAAGTCGAAC 900	601 ATCAGCTAGCGAGTTGGCTGCAGAAGCCTTCCTATCTGGTCAAGAATCTGTCAAA 6

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21335329
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Dopazo,J., Mendoza,A., Herrero,J., Caldara,F., Polissi,A., Humbert,Y., Friedli,L., Guerrier,M., Grand-Schenk,E., Gandin,C., Francesco,M., Buell,G., Feger,G., Garcia,E., Peitsch,M. and
                                                                                   and Garcia-Bustos, J.F.
Annotated draft genomic sequence from a Streptococcus
type 19F clinical isolate
Microb. Drug Resist. 7 (2), 99-125 (2001)
                                                                                                                                                                                                                    Streptococcus pneumoniae
Streptococcus pneumoniae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Streptococcus pneumoniae clone (
AL449937
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Direct Submission

Submitted (31-OCT-2000) Research Department, Gl
Severo Ochoa 2, 28760 Tres Cantos, SPAIN

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is ava

* the accession number will be preserved.

Location/Qualifiers
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                                                                                                                  CGTGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTG
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    ACATGATATAATCAGTGAAGGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCA
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/mol_type="genomic DNA"
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                                    Friedli, L., Mendoza, A., Herrero, J., Caldara, F., Humber Friedli, L., Guerrier, M., Grand-Schenk, E., Gandin, C., Francesco, M., Polissi, A., Buell, G., Feger, G., Garçia, and Garcia-Bustos, J.F.
Annotarea decer.
 Annotated draft genomic sequence from a Streptococcus pneumoniae type 19F clinical isolate Microb. Drug Resist. 7 (2), 99-125 (2001)
                                                                                                                                     Streptococcus pneumoniae
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Direct Submission
Submitted (31-0CT-2000) Research Department, Glaxo Wellcome, S.A Severo Ochoa 2, 28760 Tres Cantos, SPAIN
* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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/mol_type="genomic DNA"
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QATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYYYYNGKVPYDAIISEE
LLMKDENYGLKDEDIISEIKGGYVIKUDGKYVYYLKDAHAADNVRTKEEINGKQHHS
GHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVHGDHYYHIEK
LSASELAAAKAFLSGRGNLSNSRTYERQNSDNTSRTMWPEVSNSPGTTNTNTSNNSN
TNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLIFDPAQITTSRTANGVVPHGDHYHF
IPYSQLSPLEEKLARIIFLRYERSNHWVEDSRPEQFSPGTPEBSPSPQDAPNPQPAPS
NPIDEKLVKEAYRKVGDGYVFEENGVPRIFAFAGLASETAAGLUSKLAKQESLSHKLG
AKKTDLPSSDREFYNKAYDLLARIHQDLDDNKGRQVDFEALDNLLERLKDVSSDKYKL
VDDILAFLAPIIHPERLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPDITSDEGG
DAYVTEHMTHSHWIKKDSLSBERAAAQXXAKKGLTPPSTDHQDSGNTEAKGAEAIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                 NRVKAJAKKVELDRMPYNLQYTVEVKNGSLI I PHYDHYHNI KFEWFDEGLYEAPKGYSL
EDLLATVKYYVEHPNER PHSDNGFGNASDHVQRNKNGQADTNGTEKPEEEFDQTEKPE
EETPREEKPQSEKPESPKFTERPEESSPESPEPEDESTPQVETEKVKEKLREAEDLLGK
IQNPI I KSNAKETLTGLKNNLLFGTQDNNT I MAEAEKLLALLKESK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="phpA"
/note="histidine motif-containing protein"
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/db_xref="GI:13447094"
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/transl_table=
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Pred. No. 8.6e-96;
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                     Query Match
Best Local Similarity
Matches 148; Conserv
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Best Local Similarity
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                                                                                                                                                                      Streptococcus antigens
Patent: WO 0198334-A 4 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
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Patent: WO 0198334-A 3 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
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AX343072
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                                                                                             /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
/note="BVH-11"
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1. .2647
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
/note="BVH-11"
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Pred. No. 1e-67;
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Pred. No. 1e-67;
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AF340222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (25-JAN-2001) Department of Bacteriology, Wyeth Lederle Vaccines, 211 Bailey Road, West Henrietta, NY 14586, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein from Streptococcus pneumoniae, protects mice intranasal pneumococcal challenge Infect. Immun. 69 (6), 3827-3836 (2001)
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Zhang, Y., Masi, A., Barniak, V.,
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1 (bases 1 to 2166)
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                                                                                       YEQMSELEKRIARIIPLRYRSNHWVPDSRPEQPSPQSTPEPSPSPQPAPNPQPAPSNP
IDEKLIVKEAVRKVGDGYVFEENGVSRYIPAKOLSAETNAGIISKLAKQESLSHKLGAK
KTDLPSSDREFYNKAYDLLARIHQDLLDNKGRQVDFEALDNLLERLKDVPSDKVKLUD
DILAFIA,PIRHPERLGKRNAQITYTDDBIQVAKLAGKYTTEDGYIFDPRDITSDEGDA
YVTPHMTHSHHIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNR
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LLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKPEEE
TPREEKFQSEKEESYKPTEPEESSPEESSEEPQVETEKVEEKLKRAEDLLGKIQDPIIK
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                                                                                                                                                                                                                                                            /translation="MKDPNYQLKDSDIVNEIKGGYVIKVDGKYYVYLKDAAHADNIRT
KEEIKRQKQEHSHNHGGGSNDQAVVAARAQGRYTTDDGYIFNASDIIDTGDAYIVPH
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YHQNQGENISSLLRELYAKPLSERHVESDGLIFDPAQITSRTARGVAVPHGNHYHFIP
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                                                                                                                                                                                                                                                                                                                                   /product="PhpA-79"
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                                                                                                                                                                                                                                                                                                                                                                                                         /gene="phpA-79"
/note="N-terminal truncated PhpA protein; histidine
motif-containing protein"
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/transl_table=11
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/note="derived from Streptococcus
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L. .2166
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2e-16;
               Length 2166;
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JOURNAL
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Matches 53; Conserv
Query Match
Best Local Similarity
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                                                                                                                      G01N33/569,
PC G01N33
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AR120270
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Choi,G.H., Kunsch,C.A., Ba
Fannon,M.R. and Rosen,C.A.
                                                                                                                                                                                                                           PF PN
                                                                                                                                                                                                                                                            Streptococcus pneumoniae antigens and vaccines Patent: JP 2001505415-A 33 24-APR-2001; HUMAN GENOME SCIENCES INC
                                                                                                                                                                                                                                                                                                                                        unidentified
                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae antigens and vaccines Patent: US 6159469-A 65 12-DEC-2000;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                  Kunsch, C.A., Choi, G.H.,
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                                                                                                                                                                                                                                                                                                                                                    unidentified
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D 24-APR-2001
D 39-APR-2001
F 30-OCT-1997 JP 1998520667
R 31-OCT-1996 US 60/029960
I CHARLES A KUNSCH,GIL H CHOI,SYDNOR L JOHNSON,ALEX HROMOCKYJ C12N15/31,C12N5/18,C12N1/21,C07K14/315,C12Q1/68,A61K39/09, PC
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ilarity 100.0%;
Conservative
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                                                                                                                                   Topology: Linear;
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                                               /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
474 c 498 g 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unknown"
474 c 498 g
                                                                                                           Location/Qualifiers
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 Score 53;
Pred. No.
                                                                                                                        Location/Qualifiers.
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Pred. No.
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US 6159469
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2e-16;
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                                 STEVEN C BARASH,
PI MICHAEL FAUNCON
PC C12N15/09,A01K
PC C12N1/21,
PC C12N5/10,C12P2
G06F15/40
CC Strandedness:
CC Topology: Line
FH Key
FT Source
FT Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
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PD 1
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                                                                                                                                                                                                                                                                                                                                              unidentified
                                                                                                                                                                                                                                                                                                                                                                      JP 2001501833-A/243
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                                                                                                                                                                                                                                                                 Fannon, M. and Dougherty, B.A.
Polynucleotide of Streptococcus pneumoniae
Patent: JP 2001501833-A 243 13-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                          unidentified
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sch,C.A., Choi.G.H., Dillon,P.J., Rosen,C.A., Bara,S.C.,
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Conservative
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                                                                                                                                   MICHAEL FANNON, BRIAN A DOUGHERTY C12N15/09, A01K67/027, C07K14/315, C07K16/12, C12N1/15, C12N1/19,
                                                                                                                                                                           CHARLES A KUNSCH, GIL H CHOI, PATRICK J DILLON, CRAIG A ROSEN, PI
                                                                                                                                                                                       30-OCT-1997 JP 1998520718
31-OCT-1996 US 60/029960
                                                                                                                                                                                                                JP 2001501833-A/243
13-FEB-2001
                                                                                     Strandedness: Double;
                                                                                                                                                                                                                                                       GENOME SCIENCES INC
                                                                                                            2N5/10, C12P21/02, C12Q1/68, G06F17/30, C12N15/00, C12N5/00,
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451 c 511 g
/organism="unidentified"
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                                                  Location/Qualifiers
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Pred. No.
                                   organism='Unidentified'.
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EEPEESPEESEEPQVETEKVEEKLREAEDLLGKIQDPIIKSNAKETLTGLKNNLLFGT
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Adamou, J.E., Heinrichs, J.H.,
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amou,J.E., Heinrichs,J.H.,
     /gene="phtD"
/note="Region:
1417. .1509
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ELLMKDPNYQLKDSDIVNEIKGGYVIKVDGKYYVYLKDAAHADNIRTKEEIKRQKQEH
SHNHGGGSNDQAVVAARAQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNE
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                                                                                        /note="Region: 943. .960
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247. .264
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/transl_table=11
/product="pneumococcal
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mol_type="genomic DNA"
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RESULT 24
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Sequence 5 from Patent WO0198334
AX343074
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Sequence 1985 from Patent
AX568778
                                                                                              unidentified unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae proteins and nucleic acids Patent: WO 02077021-A 1985 03-OCT-2002; Chiron Spa (IT) ; THE INSTITUTE FOR GENOMIC RESEARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae
              Streptococcus antigens
Patent: WO 0198334-A 5 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
                                                                                                                                 unidentified
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                                                               Hamel, J., Ouellet, C.,
                                                                                                                                                                    AX343074.1 GI:18152272
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ilarity 100.0%;
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/rpt_type=direct
1597. .1779
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/note="Region: coiled-coil domain"
1678. .1695
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/gene="phtD"
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509 c 545 g 6
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2e-16;
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2e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tettelin,H., Nelson,K.E., Paulsen,I.T., Eisen,J.A., Read,T.D., Peterson,S., Heidelberg,J., DeBoy,R.T., Haft,D.H., Dodson,R.J., Durkin,A.S., Gwinn,M., Kolonay,J.F., Nelson,W.C., Peterson,J.D., Umayam,L.A., White,O., Salzberg,S.L., Lewis,M.R., Radune,D., Holtzapple,E., Khouri,H., Wolf,A.M., Utterback,T.R., Hansen,C.L., McDonald,L.A., Feldblyum,T.V., Angiuoli,S., Dickinson,T., Hickey,E.K., Holt,I.E., Loftus,B.J., Yang,F., Smith,H.O., Venter,J.C., Dougherty,B.A., Morrison,D.A., Hollingshead,S.K. and Fraser,C.M.
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53; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae TIGR4
                                                                                                                                                                                                                                                               Submitted (29-JUN-2001) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
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AE007403.1 GI:14
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ilarity 100.0%;
Conservative
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                                             /note="This region contains a match to at least one other gene that is not full length, and is not the result of a sequencing artifact; similar to GP:5019553; identified by sequence similarity; putative; IS630-Spn1, transposase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unidentified"
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/db_xref="taxon:32644"
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956. .1156
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129. 476
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                                                                                                                'gene="SP0996"
                                                                                                                                               'gene="SP0995"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (5529), 498-506 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:14972469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11931 bp
ae TIGR4
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2e-16;
                                                                                                                                                                                                                                  pneumoniae TIGR4"
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                                                                                                                                             /translation="MNI FRTKNVSLDKTEMHRHLKLWDLILLGIGAMVGTGVFTITGT AAATLAGPALVISIVISALCVGLSALFFABFASRVPATGGAYSVLYAILGEFAWLAG WLTMMEFMTAISGVASGMAAYFKGLLSQYGIAFPQALMFFNPQAGTFVDLFDILVLLVLLGVGIAHFPQALMFFNPQAGTFVDLFDILVLLVLLGVGIAHFNALSFALALFVLVGIWNIKFDNWSNFAPVGFGQIYGA STGIMAGASLMFFFFLGFESISMAVDEVKTPQKNIFRGIVLSLSIVTILYALVTLVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MKKVMFAGLSLLSLVVLMACGEBETKKTQAAQQPKQQTTVQQIAVGKDAPDFTLQSMDGKEVKLSDFKGKKVYLKFWASWCGPCKKSMPELMELAAKDDRDFELTVIAPGIQGEKTVEQFPQWFQEQGYKDIPVLYDTKATTFQAYQIRSIPTEYLIDSQKIGKIGKIQFGAISNADAEAAFKEMN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tränslation="METIVFLISVFLAGVLSFFSPCIFPLLFVYAGILLDDQESAKSF
SLFGRKVLMSGLIRTLCFIAGISLIFFILGFGAGYFGHLIYANMFRYGMGAIIIILGL
HQMEIFHLKKLEVQKSFTFKKSDSMKYWSAFLLGITFSFGMTPCIGFVLSSVLALAAS
GGNGAMQGAIYTLIYTLGMALPFLVLALASGLVMPYFSKIKRHMMLLKKIGGFLIVLM
                                                    YFTYGYKHSTIEE"
                                                                            GLIRLRKEKGMPKAGEFKTPLVPLLPILSIIICLSFMLQYNMNTWIAFLVALLVGSII
                                                                                                GVVHYSHLNVDDAVAFALRSVGISWAANYVSLVAILTLITVCISMTYALSRMIYSLAR
DGLVPAAFKELTKTSKIPKNATILTGLASAVAAGMFPLASIAAFLNICTLAYLIMLAY
                                                                                                                                                                                                                                                                             /transl_table=11
/product="amino acid permease family protein"
/protein id="AAK/55118.1"
/db_xref="GI:14972474"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GILLLLGQVNVLAGIFE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to GP:6714962; identified by sequence
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mtetnsvpagvivvsllallgviafwlirrkkeseiqqlsteli
KVLGQLDAEKADKKVLAKAQNLLQETLDFVKEENGSAETETKLVEELKAILDKLK"
                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SP1001"
3482. .4873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/trans| table=11
/product="thioredoxin family protein"
/protein_id="AAK75117.1"
/db_xref="GI:14972473"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="cytochrome c-type biogenesis protein CcdA"
/protein_id="AAK75116.1"
/db_xref="GI:14972472"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SP0999"
1833. .2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
/product="hypothetical protein"
/protein_id="AAK75115.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SP0998"
1303. .1602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="SP1001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         482.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="SP0998"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATKAVLLDAQKAPEDSALTE"
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'transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                     note="identified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      xref="GI:14972471"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   match to PFAM
                                                                                                                                                                                                                                                                                                                                                                                                                                protein family HMM
                                                    BASE COUNT
ORIGIN
Query Match
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                                                                      3963
                                                                                         /db xref="d1:14972476"
//db xref="d1:14972476"
//db xref="d1:14972476"
//tabslation="MKINKKYLAGSVAVLALSYCSYELGRHQAGQVKKESNRVSYIDG
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DQAGQKAEAULTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISE
ELLMKDPNYQLKDSDIVNEIKGGYVIKVDGKYYVYLKDAAHADNIRTKEEIKRQKQEH
SHNHGGGSNDQAVVAARAQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNE
LSASELAAAEAYWNGKQGSRPSSSSSYNANPAQPRLSENHLTVTPTYHQNQGENISS
LLRELYAKLISERHVESDGLIFDPAQITSRTARGVAVDHGNHYHFIPYEOWSELEKRI
ARIIPLRYRSNHWVPDSRPEQPSPQSTPESPSPQPAPNQPAPSNPIDEKLVKEAVR
KVGGGYVFEENGVSRYIPAKDLSAETAAGIDSKLAKQBSLHKLGAKKTDLPSSDREF
YNKAYDLLARIHQDLLDNKGRQVDFEALDNLLERLXOVPSDKVLVDDIIAFLAPIRH
PERLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDRDITSDEGDAYVTPHMTHSHW
IKKDSLSBAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDR
MPYNLQYTVEVKNGSLIIPHYDHYNN KEPENDEGLYEAPKGYTLEDLLATVKYYVEH
PNERPHSDNGFGNASSHYRKWKVDQDSKPDEDKHDEVSEPTHPESDEKENHAGLNPS
ADNLYKPSTDTEETEEEAEDTTDEAEIPQVENSVINAKIADAEALLEKVTDPSIRQNA
METITGLKSSLLLGTKDNNTISAEVDSSLLALKKESQPAPIQ"
                                                                            a
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VKDNEKVNSNVAVARSQGRYTTNDGYVFNPADI I EDTGNAYI VPHGGHYHYI PKSDLS
ASELAAAKAHLAGKNMQPSQLSYSSTASDNNTQSVAKGSTSKPANKSENLQSLLKELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mkfskkyIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDG
SQSSQKSENLTPDQVSQKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8670
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/product="adhesion lipoprotein"
/protein_id="AAK75119.1"
/db_xref="GI:14972475"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein_id="AAK75121."
/db_xref="GI:14972477"
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/transI_table=1
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/protein_id="AAK75120.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transl_table=11
product="conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="identified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="SP1003"
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     2.2%;
                                                                              2445
  Score 53;
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21.1"
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     <u>,,</u>
  Length 11931;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
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2 (bases 1 to 12372)
4 (bases 1, Alborn, W. Jr., Arnold, J., Blaszczak, L., Burgett, S., Holfins, J.A., Alborn, W. Jr., Fu, D.-J., Fuller, W., Geringer, C. DeHoff, B.S., Estrem, S., Fritz, L., Fu, D.-J., Fuller, W., Geringer, C. Glimour, R., Glass, J.S., Hann, A., Khoja, H., Kraft, A., Ladace, R., LeBlanc, D.J., Lee, L.N., Lefkowitz, E.J., Lu, J., Matsushima, P., McBlanc, D.J., Lee, L.N., Lefkowitz, E.J., Lu, J., Matsushima, P., McAhren, S., McHenney, M., McLeaster, K., Mundy, C., Nicas, T.I., McMaris, F.H., O'Gara, M., Peery, R., Robertson, G.T., Rockey, P., Sun, P.-M., Winkler, M.E., Yang, Y., Young-bellido, M., Zhao, G., Son, P.-M., Winkler, M.E., Yang, Y., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. 200k, C., Baltz, R.H., L.H., L.H., L.H., L.H., L.H., L.H., L.H., L.H., L.H., L.H., L.H., L.H., L.H.
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Streptococcus pneumoniae R6
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AE008464.1 GI:15
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                                                                                                                                                                                                                                                                                     /procein_id="aak99712.1"
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//db_xref="G1:19458515"
//tb_xref="G1:19458515"
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                                                                                                                  AKEMKDLDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIIYPHGDHHHADPIDEHKPVG
IGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNVVNLLKNSTFNNQNFTLANGQKRVS
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NERPHSDNGFGNASDHVQRNKNGQADTNQTEKPNEEKPQTEKPEEDKEHDEVSEPTHP
ESDEKENHVGLNPSADNLYKPSTDTEETEEEAEDTTDEAE I PQVEHSVI NAKI ABAEA
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VRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYI
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VGLKTLNPLESDPQNDKTYLENLEENMSILAEELK"
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3454. .8573
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1740. .2675
'gene="lmb"
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transl_table=11
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product="Pneumococcal histidine triad protein
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transl_table=
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transi_table≈11
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                     3682
                                                         983
                                                                                           53;
                                                                                                           Similarity
                                           GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1035
                                                                                         2.2%;
Carity 100.0%;
Conservative (
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precursor, truncation"
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EQRQIELALGGFTESLKKIKVS"
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EAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKPENSTDNGMLNPE
GNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGT1ELRLPSGEVI
                                                                                                                                                                                                                                                                             VKDVLTRIASALQQEKENAEQDPQTLVLYQKLYDILMSLHSYLESNNGSDADFDKVAA
LLDQLSAKSKDKTALLESTKAILVLNHQIQSKASASEETSPARNAEANGDNTSAENQP
NATAESNIETASDENKPSNTRDSKPAESTSENKTTESSTTTGNQEKPVE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (10187. .10402)
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complement(11045, .12265)
                                                                                                                                                                                                                                                            complement (11045. .12265)
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                                                                                                                                                          /gene="pepT"
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10373. .11002
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                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1/
transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="spr0912"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MFQELICLAQKTFYFFLAICRRLLVAIYHVFLKQESYNTRLQGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="spr0911"
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                                                                                         Score 53; DB 1; Li
Pred. No. 1.8e-16;
0; Mismatches 0;
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5.1"
                                                                                                                          Length 12372;
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ORIGIN
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PUBMED
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SPNEU1907/c
LOCUS
                                                                                                                              REFERENCE
AUTHORS
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SPNEU1901
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AUTHORS
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 Microb. I
21335329
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HTG; HTGS_PHASE2.
Streptococcus pneumoniae
Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
53; Conserv
                                Annotated draft genomic sequence from a Streptococcus pneumoniae type 19F clinical isolate
                                                                                    Dopazo,J., Mendoza,A., Herrero,J., Caldara,F., Humbert,Y. Friedli,L., Guerrier,M., Grand-Schenk,E., Gandin,C., de Francesco,M., Poliss,A., Buell,G., Feger,G., Garcia,E.,
                                                                                                                                                                                                                                                                               Streptococcus
AL449923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (31-CCT-2000) Research Department, Severo Ochoa 2, 28760 Tres Cantos, SPAIN NOTE: This is a 'working draft' sequence.

* This sequence will be replaced by the finished sequence as soon as it is the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dopazo,J., Mendoza,A., Herrero,J., Caldara,F., Polissi,A., Humbert,Y., Friedli,L., Guerrier,M., Grand-Schenk,E., Gandin,C., Francesco,M., Buell,G., Feger,G., Garcia,E., Peitsch,M. and
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Friedli,L., Guerrier,M., Grand-Schenk,E., Gandin,C., de
Francesco,M., Polissi,A., Buell,G., Feger,G., Garcia,E., Peitsch,M.
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                                                                          and Garcia-Bustos,J.F
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/mol_type="genomic DNA"
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* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is
* the accession number will be preserved.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae proteins and nucleic acids Patent: WO 02077021-A 4981 03-OCT-2002; Chiron Spa (IT); THE INSTITUTE FOR GENOMIC RESEARCH
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/mol type="genomic DNA"
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/clone="G54"
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/note="seq 4979 too long: 2.162.598 bases-replaced by note="seq 4979 too long: 2.162.598 bases-replaced by following seq:-seq 4979: from 0.000.001 to 0.349.980-seq 4980: from 0.300.001 to 0.649.980-seq 4981: from 0.600.001 to 0.949.980-seq 4982: from 0.900.001 to 1.249.980-seq 4983: from 1.200.001 to 1.549.980-seq 4983: from 1.200.001 to 1.549.980-seq 4984: from 1.500.001 to 1.849.980-seq 4985: from 1.800.001 to 2.149.980-seq 4986: from 2.100.001 to 2.162.598"
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/mol_type="genomic DNA"
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          1 (bases 1 to 973)
Kunsch, C.A., Choi, G.H., Dillon, P.S., Rose Fannon, M.R. and Dougherty, B.A.
Streptcocccus pneumoniae polynucleotides
Patent: US 6420135-A 355 16-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (25-JAN-2001) Department of Bacteriology, Vaccines, 211 Bailey Road, West Henrietta, NY 14586, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthetic construct artificial sequences.

1 (bases 1 to 492)
Zhang, Y., Masi, A.W., Barniak, V., Mountzouros, K.,
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Synthetic construct PhpA-20 (
AF340223
                                                                                                                                                                                      Sequence 355 from patent AR219123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein from Streptococcus pneumoniae, protects mice intranasal pneumococcal challenge Infect. Immun. 69 (6), 3827-3836 (2001)
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/transT table=11
/product="phpA-20"
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Hyhfipysqlspleeklvvlfpfvivqtigyqiqrpeqpvhnrlrepspspkpapnpq
papsnpideklvkeavrkvgdgyvfeengvaslypkprilqqkqqqalianwpsrkvy
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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9.5e-15;
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                                                                Rosen, C.A.,
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VERSION
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Sequence
AR120406
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CC Stran
CC Topol
FH Key
FT sourc
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Polynucleotide of Streptcocccus pneumoniae and sequence Patent: JP 2001501833-A 355 13-FEB-2001;
HUMAN GENOME SCIENCES INC
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ilarity 100.0%;
Conservative (
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30-OCT-1997 JP 1998520718
31-OCT-1996 US 60/029960
CHARLES A KUNSCH,GIL H CHOI, PATRICK J DILLON, CRAIG A ROSEN,
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                       Strandedness: Double;
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282 from patent US (
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178 c 211 g
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
178 c 211 g 25
                                 GI:14103982
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BD063415/c
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AR120405
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AR120405
Sequence 28:
AR120405
AR120405.1
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PC G01N33
CC Strand
CC Topolo
FH Key
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Kunsch,C.A., Choi,G.H., Johnson,S.L. and Hromockyj,A.

Streptococcus pneumoniae antigens and vaccines
Patent: JP 2001505415-A 169 24-APR-2001;

HUMAN GENOME SCIENCES INC
PN JP 2001505415-A/169
PD 24-APR-2001
PP 30-OCT-1997 JP 1998520667
PR 31-OCT-1996 US 60/029960
PI CHARLES A KUNSCH,GIL H CHOI,SYDNOR L JOHNSON,ALEX HROMOCKYJ COLNIS/31,C12N5/18,C12N1/21,C07K14/315,C12Q1/68,A61K39/09, PC
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l Similarity 100.0%;
30; Conservative
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Streptococcus pneumoniae
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Choi, G.H., Kunsch, C.A.,
Fannon, M.R. and Rosen, C
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6 c 7 g
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                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/db_xref="taxon:32644"
6 c 7 g
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   GI:14103981
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PC G01N33
CC Strand
CC Topolo
FH Key
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                         33 bp
Sequence 45 from Patent WO0198334.
AX343114
AX343114.1 GI:18152294
unidentified unidentified
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BD063414
BD063414.1 GI:22609017
JP 2001505415-A/168.
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27; Conserv
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Choi, G.H., Kunsch, C.A., Ba
Fannon, M.R. and Rosen, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unclassified.
                                                                                                                                                    Similarity
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F 31-OCT-1996 US 60/029960
I CCHARLES A KUNSCH,GIL H CHOI,SYDNOR L JOHNSON,ALEX HROMOCKYJ PC C12N15/31,C12N5/18,C12N1/21,C07K14/315,C12Q1/68,A61K39/09, PC
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llarity 100.0%;
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Conservative 0
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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AX343116.
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Local Similarity nes 25; Conserv
Streptococcus pneumoniae antigens and vaccines Patent: US 6159469-A 181 12-DEC-2000; Location/Qualifiers
                                     1 (bases 1 to 1342)
Choi, G.H., Kunsch, C.A., Ba
Fannon, M.R. and Rosen, C.A.
                                                                                                                                                                                                                                                                                             l Similarity
25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus antigens
Patent: WO 0198334-A 47 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
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Patent: WO 0198334-A 45 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
                                                                                                                                               Sequence 181 from patent AR120328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unidentified unidentified
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larity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                           /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
/note="HAMJ 284"
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
/note="HAMJ 282"
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AX608407
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                                  Glaser, P.,
                                                                        Streptococcus agalactiae
Streptococcus agalactiae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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24; Conserv
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Sequence 6336 from Patent WO02092818.
AX608407
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Streptococcus agalactiae genome sequence, use
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98
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                          Zouine, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unclassified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F 30-OCT-1997 JP 1998520667
R 31-OCT-1996 US 60/029960
I CHARLES A KUNSCH,GIL H CHOI,SYDNOR L JOHNSON,ALEX HROMOCKYJ
C12N15/31,C12N5/18,C12N1/21,C07K14/315,C12Q1/68,A61K39/09, PC
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                         Rusniok, C.,
Couve, E., B
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k; Pred. No. 0.9
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                       Poyart, C., Trieu-Cuot, P.
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                                      Lalioui, L.,
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Sequence
AX343078
         Masignani,V., Tettelin,H. and Fraser,C.
Streptococcus pneumoniae proteins and nucleic acids
Patent: WO 02077021-A 1987 03-CCT-2002;
Chiron Spa (IT); THE INSTITUTE FOR GENOMIC RESEARCH
Location/Qualifiers
1. .3117
                                                                                                                                                                                                                                                                                                                   24;
                                                                                                           Streptococcus pneumoniae
Streptococcus pneumoniae
Bacteria; Firmicutes; Lactobacillales;
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Patent: WO 0198334-A 9 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
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l Similarity 100.0%;
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llarity 100.0%;
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
/note="BVH-3"
a 398 c 505 g 665
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/mol_type="genomic DNA"
/db_xref="taxon:1311"
279 c 280 g 367
/organism="Streptococcus pneumoniae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adamou, J.E., Heinrichs, J.H., Erwin, A.L., Walsh, W., Gayle, Dormitzer, M., Dagan, R., Brewah, Y.A., Barren, P., Lathigra, Langermann, S., Koenig, S. and Johnson, S. Identification and characterization of a novel family of pneumococcal proteins that are protective against sepsis Infect. Immun. 69 (2), 949-958 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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ilarity 100.0%;
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                                 /trānslation="MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDG
SQSSQKSENLTPDQVSQKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSE
ELLMKDPNYQLKDADIVNEVKGGYIIKUDGKYVYLKDAAHADNVRTKDEINRQKQEH
VKDMEKVNSNVAVARSQGRYTTWDGYVENPADIIEDTGRAYIVPHGGHYHYIFKSDLS
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DSPSAQRYSESDGLVFDPAKIISRTPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPI
SGTGSTVSTVSTNAKPNEVVSSLGSLSSNPSSLITTSKELSSASDGYIENPKDIVEETATAY
IVRHGDHFHYIPKSNQIGQPTLPNNSLATPSPSLPINPGTSHEKHEEDGYGFDANRII
AEDDEGGFVNSHGDHNHYFFKKDLTEBQIKAACKHLEEVKTSHNGLDSLSSHEQDFYEN
AKEMKDLDKKIEEKIAGINKQYGVKRESIVNKEKNAIIFPHGDHHHADPIDEHKPVG
IGHSHSNYELFKPEEGYAKKEGNKYTGSELTNVVNLLKNSTFNNQNFTLANGQKRVS
FSFPPELEKKLGINNLVKLITPDGKVLEKVSGKVPGEGYGNIANFELDQFYLPGGTFK
FSFPPELEKKLGINNLVKLITPDGKVLEKVSGKVPGEGYGNIANFELDQFYLPGGTFK
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YTIASKDY PEVSYDGTFTVPTSLAYKWASQTIFY PFHAGDTYLRVNPQFAVPKGTDAL
VRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYI
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/transl_table=11
/product="pneumococcal histidine triad protein
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/db_xref="taxon:1313"
526 c 612 g 8
                                                                                                                                                                                                                                                                                                   /protein_id="AAK06761.1"
/db_xref="GI:12744746"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="phtE"
/note="PhtE; protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="phtE"
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|. .3120
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mol_type="genomic DNA"
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                                                                                                                                                                                                               unidentified unidentified unclassified.
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Streptococcus antigens
Patent: WO 0198334-A 1 27-DEC-2001;
Patent: WO 108334-A 1 27-DEC-2001;
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Sequence 1 from Patent WO0198334.
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/gene="phtE"
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EAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKPENSTDNGMLNPE
GNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTIELRLPSGEVI
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247. .264
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/note="BVH-3"
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1381. .1398
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1186. .1203
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1569, .1749
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1648. .1665
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 6867 bp Polynucleotide of Streptococcus
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                                                                                                                                                                                              Streptococcus pneumoniae polynucleotides Patent: US 6420135-A 192 16-JUL-2002;
                                                                                                                                                                                                              1 (bases 1 to 6867)
Kunsch,C.A., Choi,G.H., Dillon,P.S., Rosen,C.A., Barash,S.C. Fannon,M.R. and Dougherty,B.A.
                                                                                                                                                                                                                                                           Unknown
                                                                                                                                                                                                                                                                                                  Sequence 192 from patent AR218960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent: WO 0198334-A 2 SHIRE BIOCHEM INC. (CA)
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
/note="BVH-3"
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CC Stran
CC Topol
FH Key
FT Sourc
                                   Tettelin,H., Masignani,V., Cieslewicz,M.J., Eisen,J.A., Peterson,S., Wessels,M.R., Paulsen,I.T., Nelson,K.E., Margarit,I., Read,T.D., Madoff,L.C., Wolf,A.M., Beanan,M.J., Brinkac,L.M., Daugherty,S.C., DeBoy,R.T., Durkin,S., Kolonay,J.F., Umayam,L.A., Madupu,R., Lewis,M.R., Radune,D., Fedorova,N.B., Scanlan,D., Khouri,H., Mulligan,S., Carty,H.A., Cline,R.T., Gill,J., Scarselli,M., Mora,M., Iacobini,E.T., Brettoni,C., Galli,G., Mariani,M., Vegni,F., Maione,D., Rinaudo,D., Rappuoli,R., Telford,J.L., Kasper,D.L., Grandi,G. and Fraser,C.M., Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae proc. Natl. Acad. Sci. U.S.A. 99 (19), 12391-12396 (2002)
                                                                                                                                                                                                                                                                                                                    Streptococcus agalactiae 2603V/R Streptococcus agalactiae 2603V/R Bacteria; Firmicutes; Lactobacil
                                                                                                                                                                                                                                                                                                                                                                                                         AE014279.1
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Kunsch, C.A., Choi, G.H.,
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Fannon,M. and Dougherty,B.A.
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(bases 1 to 21397)
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C12N15/09, A01K67/027, C07K14/315, C07K16/12, C12N1/15, C12N1/19,
C12N1/21,
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JP 2001501833-A/192
13-FEB-2001
30-OCT-1997 JP 1998520718
31-OCT-1996 US 60/029960
CHARLES A KUNSCH,GIL H CHOI, PATRICK J DILLON, CRAIG A ROSEN,
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Location/Qualifiers
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1325 c 1212 g 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="PTS system, IIC component, putative"
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/db_xref="GGI:22534976"
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AHCLVCCVDNLWEDIKSYFQYYGCHLNHQLKLPKGAIISAKTEVYGGDFGKKNKDNV
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                                                                                                                                                                                                                                  complement (4332. .4637)
/gene="SAG1934"
                                                                                                                                                                                                                                                                                                                        ACLELFSLIGSWFIAAVEPLSQGITNFANGKMHGRRFNIGLDWPFIAGRAEIWACANI
LAPIMLVEAILLSKVGNGILPLAGIIAMGVTPALLVVTRGRLIRMITFGTLLLPLFLL
SGTMIAPFATELAKKVGAFPAGARAGSLITHSTLEGPMEKIFGYVIGKATTGQLSAII
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/gene="SAG1933"
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complement(155..2605)
/gene="SAG1932"
                                                                                                                                                                        complement (4332. .4637)
/gene="SAG1934"
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TVAIIFVGVLKIINSDLMKPTFDDLLGTGPTSPMTSTHMNYMMPIIMVLDKLFDKVF
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VLGDSDSQEKLSPPLKSEIATEENRKQANLAELNATQPNNRTTYIIPESSHSIAEQQR
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/aene="SAG1932"
                                                                                                              sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MTLTFGKPSITIRRLGVITSTYMMLGFILLCGFLHPSTIYSEEI/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /producT="neuraminidase-related protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1/
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                                                          _table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="Mlkrerlokiiekvningivtvneimeeldvsdmtvrrdldeld
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                                                                                                                                                                                                                                   /note="identified by match to PFAM protein family HMM PF02580; The product of this gene was detected by Western blot analysis. For details on the method see Tettelin et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MKRIRKSLIFVLGVVTLICLCACTKQSQQKNGLSVVTSFYPVYS
TTKAVGGDLNDIKMIRSQSGIHGFEBSSSDVAAIYDADLFLYHSHTLBAWARRLEBSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      triad family protein, complement (8936. .985
AVRKITSMRIFSDDEGKMNLSIQDIKGSVLSISQFTLFADTKKGNRPAFTGAADPVKA
                                                                                                                                                                                                                                                                                                                                                                complement (10114.
                                                                                                                                                                                                                                                                                                                                                                                                                            complement (10114. .10557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQLGIAGVSTEQEPSAKKLAEIQEFVKTYKVKTIFVEEGVSPKLAQAVASATRVKIAS
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EREFPTGLKIDLKDGTPIQYVAIPHTETQYCLVDRIFYVKNSQPITFKHMINPEEECR
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5322. .6098
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Sequence 133 from Patent WO02092818.
AX602204
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                                                                                                                                                                                                                                                          Streptococcus agalactiae genome sequence, use for developing vaccines, diagnostic tools, and for identifying therapeutic targets Patent: WO 02092818-A 133 21-NOV-2002; INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE
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Zouine, M., Couve, E., Bu
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NKYLDKKHIEEILPRVSVKSEBALYAAVGFGDLSPISINKTEKERREBERAKAKA
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DVYAMVGYIHELMRPMGGRFKDYIAAPKANGYQSIHTTYVYGPKGEIEIQIRTKEMHQV
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RIYVFTPNGAVQELPRESGPIDFAYAIHTQVGEKATGAKVNGRMVPLTAKLKTGDVVE
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DGVTKLGKVEYKSHEEQLAENHRKMLMAMSKDIRVILVKLADRLHNMRTLKHLRKDKQ
ERISRETMEIYAPLAHRLGISRIKWELEDLSFRYLNETBFYKISHMMSEKRREREELV
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complement(10567. .12783)
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                                                                  Score 24; DB 6;
Pred. No. 0.7;
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Direct Submission
Submitted (31-MAY-2002) Glaser P., Institut Pasteur,
Microorganismes Pathogenes, 25, rue du Docteur Roux,
Cedex 15, FRANCE. E-mail: pglaser@pasteur.fr Phone: +
89 96, Fax: +33 (0)1 45 68 87 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zouine, M., Couve, E., Lalioui, L., Trieu-Cuot, P. and Kunst, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glaser, P., Rusniok, C., Chevalier, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus agalactiae NEM316
Streptococcus agalactiae NEM316
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                                                                         /trānsiation="mtsvvvvgtqwgdbgkgkitdflsadaeviaryqggdnaghtiv
idnekerlhlipsgifferekisvigggvvvvprkslvvelavihgegvvtdnilaisdra
hvilpyhiklodlogdakednikigttikgigayndkaarvgiriadlldaerevaerik
kinlaeknelfekwydstplefddifeeyyeygqqikqyvtdtsvilndaldagkrvl
fegaqgvmldidqgtyffvtssnpvaggvtigsgvgbskinkvygvckaytsrygdgd
feptelfdbyggtifeigksygttylaggleggekinkvygvckaytsrygdgd
fegaptyklicvaydldgkridyypasleqlkrckpiyeelpgwseditacrsldblpen
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117. .410
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                                                                                                                                                                                                                                                                                                                                                                                      /gene="purA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="purA"
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mol_type="genomic DNA"
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NEGLENTYSQIQDKFIVKNGNMTSKDNYIVPLAMANKVVTKKILDEKHFFTPFGDBAILVEE
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VIEGTEYRFFTLEGDCIAVLERVAANNVGDGHTSGLLXKKNQNPLEGYDHSSPLEV
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IIPGFLAGYLVGFLVKMMENITPGGLDLISIIIIGAFUTRLVAKLLTPLINSTLLTIG
DILTSCAHSNPILMGIILGGTIVVVATAPLSSMALTAMLGLTGMPMAIGALSVFGSSF
MNGVLFHKLKLGSRKDNIAFASPLTCADVTSANPI PIYVTNVTVGGAACGIILTALMKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to gamma-glutamylcysteine synthetase (for
the N_terminal part) and to cyanophycinsynthetase
(C-terminal part)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="gbs1862"
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HISGRTISPLANDRILLENDING TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOT
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6700. .7518
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4324. .6576
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3465. .3470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAD47521.1"
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/db_xref="GI:24413442"
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3465. .4209 •
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'product="Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="gbs1862"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="gbs1861"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .6608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .4209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _start=1
I_table=11
                                                                                                                                                                                                                                    6608
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                                                                     RESULT 52
AC136885
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       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 24
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                                                                                                                                                                                                                                                                                                      485
   AC136885 154101 bp DNA linear F
Sus scrofa clone RP44-473J11, WORKING DRAFT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                   CGCTATACTACAGATGATGGTTAT 508
                                                                                                                                                                                                                             CGCTATACTACAGATGATGGTTAT 77473
                                                                                                                                                                                                                                                                                                                                                                    1.0%; So ilarity 100.0%; I Conservative 0;
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MAANVVKOEDTLARNIVSAEMLIEDNTKSIENLIVGVIAFIELOEFYFDSQNIEOKMDM
MAANVVKOEDTLARNIVSAEMLIEDNTKSIENLIVGVIAFIELOEFYFDSQNIEOKMDM
MAANVKOEDTLARNISAEMLIEDNTKSIENLIVGVIAFIELOEFYENASHIQGEI
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ROKLGMLRRNTIFTMKLSIAQLGMMQQSVKSGVTADAIVNANNAALQMLAETSKEAIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAYYVYDKKRLKRFTSNQRIBALKSDIKETDQDIRHLEILKKDNRSKEYIKLAHQILP
QLDLIRNEANQLQKAIBPNIYKRITKKANTFSNBINEQLIKLHASPBLBPISDQEDEM
IRIAPBLKPFYHNIQDDHFAILKKIBBADNKABLAAIHQANMKRFTDVLAGYIRIKQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="Unknown"
/protein_id="CAD47!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="gbs1866"
9770. .10747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTEEDLEKIINDSIK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEDDYKRLSEDSLAFYCDCSKERFEAALLTLGTKELQAMKDEDKGVEITCQFCNQTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="gbs1865"
8911. .9786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="gbs1864"
8911. .9786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGRKERAQLESAVIKSAETINDS
VKIRDKKIVEALLNEGKSTQEKVDES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKNFNNAKERLEQALQAIKKFNLDLDETLRQLNESDMKDFDVSLRMMQDERNSK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="gbs1866"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAD47524.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="gbs1865"
note="Similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/transl_table=11
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/note="Similar to other proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="gbs1864"
7515. .8771
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/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="Similar to transcription regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product = "Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="Unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .9786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           id="CAD47525.1"
                                                                                                                                                                                                                                                                                                                                                                        Score 24; DB
; Pred. No. 0.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other proteins"
                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
. 0.69;
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CDS RBS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a phran-derived resilies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Akhter.N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Cariaga,K., Coleman,B., Engle,J., Granite,S., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N., H.,S.-L., Idol,J.R., Karlins,E., Laric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B., Margulles,E.H., Masiello,C., Maskeri,B., McDowell,J., Paguirigan,C., Pearson,R., Portnoy,M.E., McDowell,J., Paguirigan,C., Pearson,R., Fortnoy,M.E., Schueler,M.G., Sison,C., Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Vogt,J.L., Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grovemont Circle, Gaithersburg, MD 20877, USA On Nov 26, 2002 this sequence version replaced gi:24819761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (26-NOV-2002) NIH Intramural Sequencing Center, Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-NOV-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Green, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa
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AC136885.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with a Phrap-derived quality score.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE2; HTGS_DRAFT
consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 154101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 154101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 153961 bases at least Q30
Consensus quality: 154086 bases at least Q30
Consensus quality: 154086 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                        Insert size: 148000; agarose-fp
Insert size: 154101; sum-of-contigs
Quality coverage: 12.16x in Q20 bases; agarose-fp
Quality coverage: 11.68x in Q20 bases; sum-of-cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: dbn
Center clone name: 473J11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
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VERSION
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AC137536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                   Grovemont Circle, Gaithersburg, MD 208
On Dec 18, 2002 this sequence version
                                                                                                                                                                                                                          Direct Submission
Submitted (22-NOV-2002) NIH Intramural Sequencing Center,
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 19474)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC137536 194474 bp DNA linear H
Sus scrofa clone RP44-254B17, WORKING DRAFT SEQUENCE,
                                                                                                                                          Submitted (18-DEC-2002) NIH Intramural Sequencing Center,
                                                                                                                                                                                    Green, E.D
                                                                                                                                                                                                                                                                                        Green, E.D.
                                                                                                                                                                                                                                                                                                                                                   NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Akhter, N., Antonellis, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS
                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                                                                       (bases 1 to 194474)
                                                                                                                                                                                                                                                                                                           (bases 1 to 194474)
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Contact: nisc_zoo@nhgri.nih.gov
                     Web site: http://www.nisc.nih.gov
                                        Center: NIH Intramural Sequencing Center Center code: NISC
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/note="clone overlaps with GenBank Accession Number
AC137536 clone RP44-254B17 (center project name dbo)
a 33945 c 34061 g 43739 t 1 others
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vector_side:
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/db_xref="taxon:9823"
/clone="RP44-473J11"
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                                                                                  Genome Center
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                                                                                                     gi:25700111
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E, 7 ordered
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misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 10381: contig of 10381 bp in length

* 10482 10481: gap of unknown length

* 36867 36966: gap of unknown length

* 36867 36966: gap of unknown length

* 100818 100917: contig of 63851 bp in length

* 100818 100917: gap of unknown length

* 100918 125399: contig of 63851 bp in length

* 125400 125499: gap of unknown length

* 125500 129483: contig of 3484 bp in length

* 129584 129583: gap of unknown length

* 129484 129583: gap of unknown length

* 160267 160366: gap of unknown length

* 160267 160366: gap of unknown length

* 160367 194474: contig of 30683 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     provided by the submittor
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Consensus quality: 192852 bases at least Q40
Consensus quality: 193282 bases at least Q30
Consensus quality: 193299 bases at least Q20
Consensus quality: 193599 bases at least Q20
Insert size: 175000; agarose-fp
Insert size: 193874; sum-of-contigs
Quality coverage: 12.57x in Q20 bases; sum-of-contigs
Quality coverage: 11.34x in Q20 bases; sum-of-contigs
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Center clone name: 254B17
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                                                                                                                                                                                                          36967.
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/db_xref="taxon:9823"
/clone="RP44-254B17"
                                                                /note="assembly_fragment"
125500. .129483
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   note="assembly_fragment'
129584. .160266
                                                                                                                                                                'note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                     regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abservations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSRROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 1, 2002 this sequence version replaced gi:21615720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
AL732478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL732478 203434 bp DNA linear ROD 09 Mouse DNA sequence from clone RP23-42N14 on chromosome 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                     constructed by the group of Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL732478.7
                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep
from the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                                                                    database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52095 a
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161455. .194474
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/mol_type="genomic DNP
/db_xref="taxon:10090"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160367. .194474
                                                                               organism="Mus musculus"
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                                                                                                                                     location/Qualifiers
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                                                                                                                                                                                        http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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AUTHORS
TITLE
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Best Local
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                    Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, S., Arachchi, H.M., Barna, N., Bastlen, V., Bloom, T.,
Anderson, S., Darachchi, H.M., Barna, N., Bastlen, V.,
Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,
Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,
Ferreira, P., FitzGerald, M., Gage, D., Galagan, D., Hagos, B.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Graham, L., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrin, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
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Romen, J., Change, C., Schunber, B., Camen, C., Coron, D., Rogov, P.,
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Romen, J., Change, C., Rogov, P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 214633)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren,B., Nusbaum,C. and Land
Mus musculus, clone RP24-65D16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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HTG; HTGS_PHASE1; HTGS_DRAFT
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/clone_lib="RPCI-23"
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Smith, C.
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Mar 18, 2003 this sequence version replaced gi:28195861.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currentle consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record
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Insert size: 212333; sum-of-contigs
Quality coverage: 10.6 in Q20 bases; agarose-fp
Quality coverage: 9.0 in Q20 bases; sum-of-contigs
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------ Summary Staffstics
Sequencing vector: Plasmid; n/a; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Bi
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74999: gap of 100 bp
86445: contig of 11446 bp i.
86545: gap of 100 bp
108300: contig of 21755 bp i.
108400: gap of 100 bp
127566: gap of 100 bp
127666: gap of 100 bp
127666: gap of 100 bp
182198: contig of 54532 bp i.
182298: gap of 100 bp
212649: contig of 30351 bp i.
212749: gap of 100 bp
212649: contig of 30351 bp i.
212749: gap of 100 bp
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Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFI CDNAs: Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W.,
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2 (bases 1 to 1450)

Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M. Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C. Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                       Yamada,K. (SSP/PGEC) and Seki, M. (For this work. Shinozaki,K. (RIKEN /PGEC) contributed equally to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Isi Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Tarabianki v and chicarki v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (15-MAR-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the
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                                                                                                                                                                                                                                                                                               submitted to Genbank
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/gene="At5g09300"
                                                                                                                                                        mol_type="mRNA"
db_xref="taxon:3702"
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                                                                                                         clone="U50137"
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Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-
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Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexan Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L. Full-length messenger RNA sequences greatly improve gen
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Arabidopsis thaliana clone 3693
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 1603)
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M. Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Arabidopsis Full Length cDNA Clones
The Salk, Stanford, PGEC (SSP) Consortium members carried out sequencing and annotation of the RAFI cDNAs: Yamada,K., Chan, Chang,C.H., Dale,J.M., Hsuan,V.W., R.F.,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases I to 1603)
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M.
Yamada, K.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C.
Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C.
Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y.,
Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M.,
Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P.,
Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W.,
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                                                                                                                                                                                                                      collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                               Submitted (14-FEB-2003) Plant Gene Expression Center, 800 B Street, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried out the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana
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Arabidopsis thaliana clone RAFL15-41-A11 (R50137) putative
branched-chain alpha keto-acid dehydrogenase E1 alpha subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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/db_xref="taxon:3702"
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Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to

Chan, M.M., out the

(SSP/PGEC)

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REFERENCE
AUTHORS
TITLE
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DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 59
AC015298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481
                                                                                                                                          HTG; HTGS PHASE2.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Drosophila melanogaster

Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
Rockville, MD, USA
This sequence was identified as CDM:10213547 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    this work.
                                                                           Direct Submission Submitted (16-NOV-1999) Celera Genomics,
                                                                                                                                                                                                                                                                                                 AC015298.1 GI:6436037
                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster,
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                                                                                                                             Adams, M. and Venter, J.C.
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ilarity 100.0%;
Conservative (
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/protein_id="AdA2286.1"
/protein_id="AdA2286.1"
/db_xref="G1:28393751"
/translation="MALHLRSSFSSKSTLLNILRHNLGFGSRSHYTRHIRQILPHDPP
/translation="MALHLRSSFSSKSTLLNILRHNLGFGSRSHYTRHIRQILPHDPP
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LRGSQNPISRLCNTMAEPETLSSFYQHEYANNHQWNDFPGGKVAFTPEIQFSDKE
RVPCYRVLDDNGQLITNAGPVQVSEEVAVKIYSDMVTLQIMDNIFYEAQRQGRLSFYA
RVPCYRVLDDNGQLITNAGPVQVSEEVAVKIYSDMVTLQIMDNIFYEAQRQGRUSFYGKGRQ
MPVFGSNKLNVFTVSATIATQLPNAVGAAYSLKMDKKDACAVTYFGDGGTSEGDFHA
ALNIAAVMEAPVLFICRNNGWALSTFTSDQFRSJGVVVGGRAYGIRSIRVDGNDALAM
YSAVHTAREMALREQRFILIBALTYRVGHHSTSDDSTRYRSAGEIEWNNKARNELSRF
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/note="artifact within poly A tail"
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67. .1485
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/note="This clone is in a modified pBluescript vector2
(lambda PS) as a BamHI/XhoI insert.
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/mol_type="mRNA"
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AL391712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
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/translation="MGTKQPRNYRRRCNDEIDGEDATAAAKPSSSDLYPAKPSSSDLY
PWKRRKLPAIPTKNDDDAKGRDHAKSSWLLDLSRGDEFYTQEQMQQRLKEHSQDERPM
EIVFNGERVRSIGMDGLSYVFVCPMPQTADDKMAALDRICNAYDERVNSRMPQEQPQM
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/mol_type="genomic DNA"
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chromosome="5"
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variety="Columbia"
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/gene="T5E8_20" /gene="T5E8_20" /gene="T5E8_20" /gene="T5E8_20" /note="Contains Prokaryotic membrane lipoprotein lipid /note="Contains Prokaryotic membrane lipoprotein lipid /noten site AA454-464" /codon_start=1 /product="amino acid transport protein AAP2" /protein id="CAC05448.1" /protein id="CAC05448.1" /db_xref="d1:995509" /db_xref="d1:995509" /db_xref="d1:995509" /translation="MGETAAANNHRHHHHHGHOVFDVASHDFVPPQPAFKCFDDDGRL /krigtywhashliTaVaIGSGYLSLAWAIAQLGWIAGFAWMLLFSLVTLYSSTLLSDC YRTGDAVGGKRYTYNDAVRSILGGFREKICGLIQVLNHLFGIAIGYTIAASISIMAIK RSNCFHKSGGKDPCHMSSNPYMIVFGVAEILLSQVPDFDQIWWISIVAAWSFTYSAI GLALGIVQVAANGVFKGSLTGISIGTYTQTOKIWATFQALGDIAFAYSYSVULLEIQD TVRSPPAESKTMKKATKISIAVTTIFWLCGSMYAAAFGDAAPGULTGFGFYNPFWL LDIAWAAIVHLUGAYQVFAQDIFAFIEKSVAERYPDNDFLSKEFEIRIPGFKSPYKV NVFRNVYRGGFVVTTTYVISMLMPFFNDVYGILGALGFWPLTTYFFVEMYIKQRKVEKW STRWVCLQMLSVACLVISVVAGVGSIAGVMLDLKVYKPFKSTY"	/gene="T558_20" join/7652.	Complement (55685634) Complement (55685634) Complement (56356144) Complement (56356144) Gene="T5E8_10" Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Complement (56356144) Co	complement (53985441) /gene="TSE8 10" /number=6 complement (54425567) /gene="TSE8 10" /number=7	/gene="T5E8_10" /gene="T5E8_10" /number=5 /gene="T5E8_10" /gene="T5E8_10" /number=6	/number=4 complement(49105226) /gene="T5E8_10" /number=5 complement(5227 5274)	Complement (44124685) /gene="T588_10" /number=4 complement (46864909) /gene="T5E8_10"		/ Indimode = (100	5E8_10" 1 nt(3525 5E8_10"	LPHVBSIASESNIHDAVTKTERIVASISGVWTGPSVTRTHSHLLQPLVDCTLTLGRIL EKKVCLGTGRYGNHWSRPQEDVDLQLTDPFSVRIKVI" complement (395. 3451) /gene="T5B8_10" /number=1 complement (34523524)	YAGRPEELAKEPDENLIMSIAAAESCPSAPVYKYASLQEISDFKSVFRNFMQGICVAF VCVSCAFISIKRLLSIFFLSOKNGYLITAIEDOMKVDGYSLIVEGDSSTDDESDCETS AYEEARDSLLQRADKIFSDASVVYSELSRVKSIFKRGARHPSPAFRAAYTSLTVPSMY SPYLRLELLRWDPLHQDVDFSDMNWHGLLFHSRIVCGSFPVCTNVNFVSELVKVVAVP ILHRIVRCWDILSTRETRNVVAATSLVARYVFPSEALLAELSLAIHARLVEAIIAIS VPTWDDQVSKUVPNAPQVAAYRFGTSVELMRNICMWKDVMELFYLEKLALSDLLFGKV
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Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garria, M., Garra, M., Gebregoergis, E., Geer, K., Gill, R., Grady, M., Garra, M., Guevara, W., Gluevara, M., Handerson, M., Hernandez, M., Guevara, W., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hiladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hilyk, S., Khan, Z., King, L., Kowar, C., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kowar, C., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kowar, C., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kowar, C., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kowar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Longacre, S., Lopez, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lovando, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Manja, B., Mortins, S., Murphy, M., Nair, L., Mangum, M., Malloy, K., Mangum, A., Mankervis, C., Neal, D., NewCon, N., Nguyen, N., Norris, S., Naveris, S., Muridasa, M., Murphy, M., Nair, L., Nackelmeh, O., Okwuonu, G., Olarmpunsagoon, A., Pal, S., Parks, K., Pal, S., Pall, H., Perez, A., Perez, L., Pfannkoch, C., Parks, K., Reilly, M., Ren, Y., Router, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Parks, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, O.D., Smajs, D., Shen, H., Shetty, J., Shora, R., Walter, B., Wang, J., Wallson, R., Walter, B., Wang, J., Wallson, R., Walter, R., Woden, H., Worley, K., Willson, R., Walter, R., Wolden, H., Worley, K., Wallson, R., Walter, R., Wolden, H., Worley, K., Wallson, R., J., Yoon, V., Wallson, L., Yoon, V., Wallson, L., Yoon, V., Wallson, L.
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Allen, C., Alger, M., Baca, E., Baden, H.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Bhair, J., Blankenburg, K., Byth, P., Brown, M.,
Bryant, N., Catter, K., Cavzcos, I., Ceassar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Chacko, J., Chavez, D., Chen, G., Coyle, M., Cree, A., D'Souza, L.,
Chacko, J., Chavez, D., Davy-Carroll, L., De Anda, C., Dederich, D.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Bagan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Farnana, R., Escotto, M., Sigene, C., Evans, C.A., Falls, T., Fan, G.,
Farnana, R., Escotto, M., Sigene, C., Evans, C.A., Falls, T., Fan, G.,
Farnana, M., Farnana, R., Farnana, M., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R., Farnana, R
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AC123445.4 GI:25137917
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158501 bp DNA linear HTG 20-NOV-: Rattus norvegicus clone CH230-403G9, *** SEQUENCING IN PROGRESS ****, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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12990. .13089
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100.0%; Pred. No.
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REFERENCE
AUTHORS
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JOURNAL
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TITLE
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                                                                                                                                                        misc_feature
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                                                                                                                                                                                                                                                                                                                           source
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On Nov 20, 2002 this sequence version replaced gi:23907751.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.)
NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project Information
Center project name: GXID
Center clone name: CH230-403G9
Center clone name: CH230-403G9
Center clone name: CH230-403G9
Center clone name: CH230-403G9
Consensus quality: 159374 bases at least Q40
Consensus quality: 169374 bases at least Q30
Consensus quality: 16918 bases at least Q20
Estimated insert size: 162538; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                    165393
166780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Baylor College of Medicine Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                  /note="wgs_end_extension clone_end:Sp6"
/note="wgs_end_extension
clone_end:Sp6"
                                                                  2097.
                                                                                                                                                                                                                       /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                           1. .168601
                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                             clone="CH230-403G9"
                                                                                                                                                                                                                                                                                                                                                                             165292: contig of 165292 bp in length 165392: gap of unknown length 166779: contig of 1387 bp in length 166879: gap of unknown length 168611: contig of 1722 bp in length.
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REFERENCE
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VERSION
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AC007811/c
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                                                                                                                                                Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Classiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacaleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                    Submitted (14-JUN-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Feb 15, 2001 this sequence version replaced gi:5822638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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22; Conserv
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1 (bases 1 to 171569)
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Berkeley Drosophila Genome Project
                      Sequence submitted by:
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complement(160964..16:
/note="clone_boundary
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clone_end:Sp6"_
9046._.10005
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                                                                                                                                                                                                      Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: RMBL; Sw.: SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10
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AL117340.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 30, 1999 this sequence version replaced gi:5931851.
During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 187517)
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                                                                                            Contact: humquery@sanger.ac.uk
                                                                                                                  Web site: http://www.sanger.ac.uk
                                                                                                                                             Center code:
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/clone lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
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RP11-192P3 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198084 bp DNA linear
Homo sapiens BAC clone 13d21, complete sequence.
AF225898
                                                                                                                                                                                                                                                                                                                                     Submitted (18-JAN-2000) Department of Human Genetics, Merck & Inc, SumneyTown Pike, West Point, PA 19486, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fitzpatrick, E.S., Hammond, H.A., DeAngelis, D.M., Soderman, A.R.,
Wright, J.L., Liu, X., Diane, L., McGowan, J., Ziegler, S., Hess, J.F.,
Todd, J., Caskey, C.T. and Metzker, M.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                    Fitzpatrick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens Chromosome 10 BAC clone b13-d-21
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/db_xref="taxon:9606"
/chromosome="10"
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/clone_lib="RPCI-11.1"
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join[98048...98249,132795...132849,139367...139528,
147695...147897,151625...151730,157139...158949,
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Accession Number U19969"
                                                                                                                          /standard_name="Z23391"
97612. .97702
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/rpt_family="Alu"
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69332. .69591
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/rpt_family="L1"
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147695. .147897,151625. .151727,157139. .158949,
160946. .161126,163685. .164393)
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160946. .161126,163685. .164819)
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|71783. .172068
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/note="corresponds to mRNA sequence deposited in
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complement (184171 . .184684)
/rpt_family="THE1"
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181649. .182174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (13-FEB-2003) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA Sequence update by submitter On Sep 18, 2002 this sequence version replaced gi:10726587.
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Submitted (06-SEP-2002) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
6 (bases 1 to 212941)
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/note="last curated on Mon Aug
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3241. .3399,3454. .3773,3829. .4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome="3R"
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                            gene="pxt"
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                                                                                                                                                                                                                 50. .2552,2615. .2942,3004.
.4066)
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                                                                               .2486,2615. .2942,3004. .3178,
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HDYNVNVNPAITNEFSGAAYRMGHSSVDGKFQIRQEHGRIDEVVNIPDVMFNPSRMRK
REFYDDMLRTLYSQEMQQVDSSISQGLSRFLFRGDNPFGLDLAAINIQRGRDQGLRSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQKLSRVYRTÞDDIDLMVGGLLEKAVEGGVVGVTFABILADQFARFKGGRYYYEYDN
GINPGAFNPLQLQBIRKVTLARLLCDNSDRLTLQAVPLAAFVRADHPGNQMIGCDDPN
LPSVNLBAWRA"
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E11ADQFARFKQGDRYYYEYDNGINPGAFNPLQLQEIRKVTLARLLCDNSDRLTLQAV
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LVQCCSPEGKVALSPQQSHFACMPIHVEPDDEFFSAFGVRCLNFVRLSLVPSPDCQLS
YGKQLTKVTHFVDASPVYGSSDEASRSLRAFRGGRLMMNDFGRDLLFLTNDKKACPS
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complement(5533. .6153)
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Reilly, B., Reilly, M., Ren, Y., Reuves, K., Regier, M.A., Reigh, R., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Socelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Wang, J., Wallson, R., Wleczyk, R., Wooden H., Walte, F., Williams, G., Willson, R., Wleczyk, R., Wooden H., Wang, J., Williams, G., Willson, R., Wleczyk, R., Wooden H., Wang, J., Williams, G., Willson, R., Wleczyk, R., Wooden H., Wang, J., Williams, G., Willson, R., Wleczyk, R., Wooden H., Wang, J., Williams, G., Willson, R., Wleczyk, R., Wooden H., Wang, J., Walliams, G., Willson, R., Wleczyk, R., Wooden H., Wang, J., Walliams, G., Willson, R., Wleczyk, R., Wooden H., Wang, J., Walliams, G., Willson, R., Wleczyk, R., Wooden H., Wang, J., Walliams, G., Willson, R., Wleczyk, R., Wooden H., Wang, J., Walliams, G., Willasana, D., Walliams, R., Williams, G., Willson, R., Wleczyk, R., Wooden H., Wang, J., Walliams, G., Willson, R., Wleczyk, R., Wooden H., Wang, J., Walliams, G., Willson, R., Wleczyk, R., Wooden H., Wang, J., Walliams, G., Willasana, M., Walliams, G., Willasana, M., Walliams, G., Willasana, M., Walliams, G., Walliams, G., Walliams, R., Walliams, R., Walliams, G., Walliams, G., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Walliams, R., Wa
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Bena
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
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Rattus norvegicus clone CH230-166D21, WORKING DRAFT SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
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/note="last curated on Mon Jan 21 21:08:19 PST 2002"
/map="90C2-90C2"
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7.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:25089200.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (05-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Center project name: GINS
Center clone name: CH230-166D21
Center clone name: CH2210-166D21
Center Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 213950 bases at least Q40
Consensus quality: 215107 bases at least Q30
Consensus quality: 215107 bases at least Q20
Consensus quality: 215809 bases at least Q20
Estimated insert size: 225832; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Baylor College of Medicine Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                  Project Information
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BASE COUNT ORIGIN FEATURES source misc_feature NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 221952: contig of 221952 bp in length. 63742 end_sequence:BH279251" 47344 c 43902 g 61410 t site: EcoRI complement (217689. .218272) /note="clone_boundary clone_end:T7 /clone="CH230-166D21" organism="Rattus norvegicus" /mol_type="genomic DNA" db_xref="taxon:10116" location/Qualifiers .221952

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DEFINITION
ACCESSION
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                                      Allen, C., Allen, H., Albirocks, S., Amin, A., Adams, C., Allen, J., Allen, C., Allen, H., Albirocks, S., Amin, A., Angulano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Badden, H., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Badden, H., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Badden, H., Baldwin, D., Bandzer, M., Baristead, M., Benahmed, F., Blawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Belahwell, R., Caracos, I., Caderon, E., Chu, J., Claveland, C., Cockreil, R., Caracos, I., Caderon, E., Chu, J., Cleveland, C., Cockreil, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., L., Davis, C., Davy-Carroll, L., De Anda, C., Dedarch, D., Delgado, O., Denson, S., Dermo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Goler, F., Chu, J., Laco, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Fersear, C.M., Gabisi, A., Ganta, R., Garria, A., Garner, T., Garza, M., Gebregoergis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guerra, W., Ghara, P., Hadden, S.L., Hodgson, A., Hogues, M., Hernandez, R., Hines, S., Haldun, S.L., Hodgson, A., Hogues, M., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Horuse, M., Hallins, B., Johnson, A., Warse, C., Karpathy, S., Kelly, S., Kelly, S., Kaln, Z., King, L., Kovar, C., Kowals, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Loudon, P., Longaere, S., Lopez, J., Liu, J., Liu, W., London, P., Longaere, S., Lopez, J., Liu, J., Liu, W., London, P., Longaere, S., Lopez, J., Liu, J., Liu, W., London, P., Longaere, S., Lopez, J., Liu, J., Liu, W., Loudon, P., Longaere, S., Lopez, J., Liu, J., Liu, W., Loudon, P., Longaere, S., Lopez, J., Liu, J., Liu, J., Liu, J., Loudon, P., Longaere, S., Lopez, J., Louses, J., Marten, M., Martin, K., Martin, K., Martin, K., Martin, K., Martin, K., Martin, K., Martin, K., Waldron, 
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
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100.0%; Pred. No. 7.8;
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318 TTATCAAGGTAGATGGAAAATA 339
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of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:25089200.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas:
assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
          l Similarity
22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Molecular and Human Genetics, Baylor
Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.h NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
1 221952: contig of 221952 bp in length.
Location/Qualifiers
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Center clone name: CH230-166D21

Center clone name: CH230-166D21

Center clone name: CH230-166D21

Center Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 213950 bases at least Q40

Consensus quality: 215107 bases at least Q40

Consensus quality: 215107 bases at least Q20

Consensus quality: 21509 bases at least Q20

Estimated insert size: 225832; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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/note="clone_boundary
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47344 c 43902 g 61
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                                                                    Submitted (13-NOV-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
On Nov 13, 2002 this sequence version replaced gi:23322375. The sequence in this assembly is a combination of BAC based 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                              Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burke, F., Burkett, C., Burrell, K.L., Byrd, N.C., Burhay, C., Burkett, C., Burrell, K.L., Byrd, N.C., Burkett, C., Burrell, K.L., Byrd, N.C., Burkett, C., Burrell, K.L., Byrd, N.C., Burkett, C., Burrell, K.L., Byrd, N.C., Burkett, C., Burkett, C., Burrell, K.L., Byrd, N.C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., 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Rattus norvegicus (Norway rat)
Rattus norvegicus
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Direct Submission
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231485 bp DNA linear HTG 13-
Rattus norvegicus clone CH230-2118, WORKING DRAFT SEQUENCE
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Nov 13, 2002 this sequence version replaced gi:23322375. sequence in this assembly is a combination of BAC based reads whole genome shotgun sequencing reads assembled using Atlas
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                                                                           RESULT 69
AX343113
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NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       provided by the submittor.

This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 231485: contig of 231485 bp in length.
                                                      CTAACACAAGCAACAACAGCAA 768
CTAACACAAGCAACAACAGCAA 132682
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------ Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 21236 bases at least Q40
Consensus quality: 212916 bases at least Q20
Consensus quality: 214916 bases at least Q20
Consensus quality: 216847 bases at least Q20
Estimated insert size: 219119; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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clone_end:T7"
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complement(228332.
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142856. .144354
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|mol_type="genomic DNA"
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AX343113

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PAT 12-JAN-2002

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Patent: WO 0198334-A 44
SHIRE BIOCHEM INC. (CA)
                                                                                                                                                                                                                                                   Original source text: Simian immunodeficiency virus (individual_isolate Mne) DNA.

Location/Qualifiers
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Overbaugh, J. and Rudensey, L.M.
Alterations in potential sites for glycosylation predominate evolution of the simian immunodeficiency virus envelope gene
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/isolate="Mne"
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AC014153/c
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                                                 Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda;
Neoptera; Endopterygota; Diptera; Brachyce
                                                                                                                             AC014153.1 GI:64
HTG; HTGS_PHASE2.
                                                                                                                                                                                AC014153 bp DNA Drosophila melanogaster, *** SEQUENCING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Solanum tuberosum BEL1-related homeotic protein 30 (Bel30) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (07-AUG-2001) Department of Horticulture, University, 257 Horticulture Hall, Ames, IA 50011-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen, H., Rosin, F.M
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eu Asteridae; lamids; Solanales; Solanaceae; Solanum.

1. (bases 1 to 2065)
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 Adams, M.
               Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                     AC014153
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A KNOX protein of potato interacts with several members of the TALE family of transcription factors
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n,H., Rosin,F.M. and Hannapel,D.J.
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and Venter, J.C
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KPMVEEMYKBEAGDAKIDSNSSSDVAPRLATKDSKVEERGELHQNAASEFEQYNSGQI
LESKSNHEADVEMEGASNAETQSQSGMENQTGEPLPAMDNCTLFQDAFVQSNDRFSEF
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CLRDAICDQIRASRRSLGEQDASENSKAIGISRLRFVDHHIRQQRALQQLGMMQQHAW
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YSSSGAYSDWLTGTSQQQHKCIDIPSJGATPFNTSQQEILSNLGGSQMGJQDFSSWRD
SRNEMLADNYFQVAQNYGQGCLSLSLGSNIPSGIGISHYGSQNPNQGGGPMMSFRODD
NSQPKEQRNADYFPPDNPGRDLDAMKGYNSPYGTSSIARTIPSSKYLKAAQYLLDEVV
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/db_xref="taxon:4113"
1. _2065
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/product="BEL1-related homeotic
/protein_id="AAN03627.1"
/db_xref="GI:22652127"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Solanum tuberosum"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      For further information on this sequence e-mail to fly@ce.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
                                                                                                                                        Insert size: 56408; sum-of-contigs
Insert size: 186298; 2.8% error; agarose-fp
Quality coverage: 1.39x in Q20 bases; sum-of-contigs Quality
coverage: 0.90x in Q20 bases; agarose-fp
                                                                                                                                                                                               Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 34830 bases at least Q30
Consensus quality: 39888 bases at least Q30
Consensus quality: 46207 bases at least Q20
                                                                                                                                                                                                                                                                                                 Direct Submission

Simple of the May 2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                        Center project name: zKp69C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 58408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX510940 S8408 bp DNA linear HTG 17-MAY-2003 Danio rerio clone DKEYP-69C1, *** SEQUENCING IN PROGRESS ***, 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
                                                                                                                                                                                                                                                                                                                                            Center code: SC
                                                                                                                                                                                                                                                                                                                                                          Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                         On May 19, 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sims, S.
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           NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/mol_type="genomic DNA"
/mbl_type="genomic ZNA"
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5972 c 6050 g 8602 t
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2066: contig of 2066 bp in length
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Pred. No.
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Ostariophysi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to fly@celera.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the submitter.
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6849
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              /note="assembly_fragment:00221"
29463. .32085
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fragment_chain:2"
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                                           /note="assembly_fragment:00208"
26893. .29362
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fragment_chain:2"
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fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/db_xref="taxon:7955"
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note="assembly_fragment:00292"
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fragment_chain:1"
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58408: contig of 2
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gap of 100 bp
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AC120849
AC120849.1 GI:20531830
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (13-MAY-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
----- Project Information
Center project name: L19545
Center clone name: 342_0_10
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Genome

Submitted (13-MAY-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html Center: Whitehead Center code: WIBR Genome Center Institute/ MIT Center for Genome Research

Web site: http://www-seq.wi.mit.edu

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* NOTE: This record contains 86 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSEROT: TT., TRAMBL: Wo:, WORMPEP: Information on the WORMPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Draft Sequence Produced by Genome Therapeutics Corp, 100
Street, Waltham, MA 02453, USA
http://www.genomecorp.com
                                                                                                                                                                                               RP11-344N10 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                       SWISSPROT; {\tt Tr:}, {\tt TREMBL}; {\tt Wp:}, {\tt WORMPEP}; {\tt Information} on the WORMPEP database can be found at
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TITLE
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Best Local
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                                                                                           Submitted (03-FEB-2000) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis, ----- Genome Center
                                                                                                                                                               Submitter:
University, 4444 ...
'hases 1 to 133237)
                                                                                                                                                                                                              Direct Submission
Submitted (27-AUG-1998)
                                                                                                                                                                                                                                           2 (bases 1 to 133237) Waterston, R.
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Andrews, S., Lacy, M. and Dubbelde, C.
The sequence of Homo sapiens PAC clone RP4-620P6
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                   Direct Submission
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21; Conservative
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41513 a 25955 c 24645 g 37446 t
Center project name: H_DJ0620P06
               Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
                                                              Center: Washington University Genome Sequencing Center code: WUGSC
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                                                                                                                                                                                                Department of Genetics, Park Avenue, St. Louis,
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

such as compressions and repeats; all regions sequence from more than one subclone; and the all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems. confirmed by restriction digest. This sequence was finished as follows unless otherwise noted: were covered assembly was

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at Roswell Park Cancer Institute, using the method described by Ioannou et al., Nature Genetics

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FEATURES
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Location/Qualifiers
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complement (2910. .387)

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/protein_id="AAC33152.1"
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mol_type="genomic DNA"
db_xref="taxon:9606"
chromosome="7"
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complement (60329. 60653)
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40647. .40946
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34916. .35207
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                                                                                                                                                                        db_xref="GI:485254"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="match to EST F06363
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705. .74929
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b_xref="GI:1254905"
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                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                    NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 139357)
Du,H., Haakenson,W. and Dixon,R.
The sequence of Homo sapiens BAC clone RP11-568H24
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6: On Aug 28, 2001 this sequence version replaced gi:13399437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 (bases 1 to 139357)
Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-SEP-1999) Genome University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 119357)
Sulston, J.E. and Waterston, R.
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                                                                                  MAPPING INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (28-AUG-2001) Genome
                                         McPherson,
                                                          Mapping information for this clone was provided by Dr.
                                                                                                                        restriction digest.
                                                                                                                                                                                                                                                                                   between neighboring data submissions.
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Homo sapiens BAC clone RP11-568H24
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                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: H_NH0568H24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center Center code: WUGSC
erson, Department of Genetics, Washington Universit For additional information about the map position ence, see http://genome.wustl.edu/gsc
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University, St. :
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SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial arrificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
VECTOR: pBACe3 6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP11-178E6, 2000 bp overlap.
Actual start of this clone is at base position 1 of RP11-568H24.
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The sequence between 66093 to 66578 and 104506 to 104590 is covered only by per products from clone DNA. he sequence contains a dinucleotide (TG) run from 65513 to 65634 in which the exact length is unknown. The sequence contains a dinucleotide (TC) run from 104386 bp to 104631 bp in which the exact length is unknown. The sequence from base position 4458 to 6187 can not be guaranted due to a tandem repeat.

Location/Qualifiers

1.139357

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repeat_region
                                                                                                                                                                                                                                                       /rpt_family="Alu"
3182 voc
                                                                                                                                                                                                                      /note="similar to (NID:g12685340)"
                                                                                          note="CpG_island (%GC=74.6,
1978. .5152
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/clone_lib="RPCI-11"
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                                                                                                                                                                                                                                                                                                                                              note="similar to Homo sapiens EST AI597790 (NID:g4606838)
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                                          _family="SVA"
                                                                       _family="(CCGG)n"
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              _family="GC_rich"
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                                                                                                      o/e=0.80, #CpGs=159)"
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21-AUG-2002 15

Ali,A., Allen,N., iy,L., Boukhgalter,B.,

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                                                                     CAGATGTTAAAGCAAATCCAA 47614
                                                                                                                                                                                                Conservative
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9239. .9360
                                                                                                                                                                                                                                                                                                                                                         9322. .9360

/note="similar to Homo sapiens

(NID:911259616)"

9333. .9360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to Homo sapiens (NID:914653314)" 9322. 9360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9240.
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/note="match to EST BF314952
9031. .9360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="SVA" 6443. .6529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9322. .9360
/note="match to EST BI198782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="GA-rich"
6531. .6732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to Homo (NID:g14653329)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9068. .9069
                                                                                                                                                                                                                                                                                                                           note="match to EST BE313758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="similar to Homo sapiens (NID:g11264380)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="match to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="match to
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/note="match to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="match to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _family="L1"
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                                                                                                                                                                                                                           Score 21; ; Pred. No.
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                                                                                                                                                                                                Mismatches
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28;
                                                                                                                                                                                                                                                                                                                    (NID:g9134050)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NID:g14653803)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NID:g11099821)"
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                                                                                                                                                                                                                                                         Length 139357;
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VERSION
KEYWORDS
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AUTHORS
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AUTHORS
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LOCUS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
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                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marguis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigillo, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                            McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., VO, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Goyd, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T., Labore, R., Landers T
                                                                                                                                                                                      Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:17061340. All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazzaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Farreira,P., Fitzcerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Ferreira,P., Fitzcerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., MacConald,P., Major,J., Matthews,C., MacConald,P., Major,J., Matthews,C., MacConald,P., Major,J., Matthews,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 146690)
Birren, B., Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Mus musculus (house mouse)
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Mus musculus clone RP24-181A10,
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                 Center code: WIBR Web site: http://v
      Contact: sequence
                                                                                         Center: Whitehead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 Charles Street, Cambridge, MA 02141,
http://www-seq.wi.mit.edu
sequence_submissions@genome.wi.mit.edu
                                                                                                Institute/ MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Lander, E.
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Anderson, S.,

RESULT

for Genome

Research

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        62868
62968
78985
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Consensus quality: 142759 bases at least Q40
Consensus quality: 144340 bases at least Q30
Consensus quality: 144347 bases at least Q20
Insert size: 151000; agarose-fp
Insert size: 14520; sum-of-contigs
Quality coverage: 7.1 in Q20 bases; agarose-fp
Quality coverage: 7.4 in Q20 bases; sum-of-contig
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Center clone name: 181 A_10
----- Summary Statistics
Sequencing vector: Plasmid; n.
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1292
2634
2734
5385
5485
                                                                                                                  /note="assembly_fragment"
9799. .14648
                                                                                                                                                           5485.
  /note="assembly_fragment'
24926. .30955
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                             /note="assembly_fragment"
14749. .19191
                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP24-181A10"
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                                                     note="assembly_fragment"
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47862: gap of 100 bp
62867: contig of 15005 bp in length
62967: gap of 100 bp
78994: contig of 16017 bp in length
79084: gap of 100 bp
100397: contig of 21313 bp in length
100497: gap of 100 bp
123488: contig of 22991 bp in length
123588: gap of 100 bp
146690: contig of 23102 bp in length
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gap of 100 bp
contig of 1342 bp in length
gap of 100 bp
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gap of 100 bp
contig of 6566 bp in length
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gap of 100 bp
contig of 4443 bp in length
gap of 100 bp
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                                                                                                           Sequencing vector: M13; 0% Sequencing vector: plasmid; 100% Sequencing vector: plasmid; 100% Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of reAssembly program: Phrap; version 0.990319 Consensus quality: 126050 bases at least Q40 Consensus quality: 130849 bases at least Q30 Consensus quality: 134078 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-DEC-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC104074.1 GI:17227276
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome UNK clone RP11-370G4, WORKING SEQUENCE, 45 unordered pieces.
                                                                                                                                                                                                                                                                                                           Center project name: H_NH0370G04
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Unpublished
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Waterston, R.H.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                         Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                          Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
NOTE: This is a 'working draft' sequence. It currently consists of 45 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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37722. .47762
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31056. .37621
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/note="assembly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cambridgeshire, CBIO ISA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 21, 2002 this sequence version replaced gi:16973010.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em. ENBL; Sw.,
SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                sections only once, except for a short overlap.
The true left end of clone RP3-322L4 is at 148973 in this sequence
The true right end of clone RP1-135L22 is at 2000 in this sequence
                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
RP11-204E9 is from the library RPC1-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL512380 150972 bp DNA linear PRI 13-MAR-200:
Human DNA sequence from clone RP11-204E9 on chromosome 6, complete
                                                                                                                                                                                                 IMPORTANT: This sequence is not the entire insert of clone RP11-204E9 It may be shorter because we sequence overlapping
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1 (bases 1 to 150972)
                                                                                                                                                                                                                                                                             VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                          http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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Conservative 0; Mismatches
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45206. .47390
/note="assembly_name:Contig46"
47491. .50220
/note="assembly_name:Contig47"
50321. .53147
                                                             Location/Qualifiers
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55462. .58103
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53248. .55361
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                                                                                                Direct Submission
Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 M
Drive, Walnut Creek, CA 94598, USA
On Sep 6, 2001 this sequence version replaced gi:11465049.
                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (30-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
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                                Draft Sequence Produced by DOE Joint www.jgi.doe.gov
                                                                                                                                                                                                                                     Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 156105)
DOE Joint Genome Institute and Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (12-JAN-2000) Production Sequencing
Genome Institute, 2800 Mitchell Drive, Walnut
3 (bases 1 to 156105)
DOE Joint Genome Institute and Stanford Human
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1 (bases 1 to 156105)
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AC020977
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short insert library derived from a single pUC clone.
Restriction digest data confirm the assembly."
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be approximately 500bp by restriction digest data."
123937. .124025
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restriction digest data."
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(AL035604). Assembly confirmed by restriction dige
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/db_xref="taxon:9606"
/chromosome="6"
Completed at Stanford Human Genome Center
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CE 2 (bases 1 to 156526)

RS Worley, K. C., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Blabrooks, S.L., Amaratunge, H.C., Are, J.R., Bannin, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Bimage, K., Brown, E., Brown, B., Bryant, N.P., Buhay, C., Bwie, S., Brieva, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byd, N.C., Carron, T.F., Cartear, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chondhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Cyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falla, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackboon, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovah, J., Kurshi, A., Landry, N., Leal, B., Lewis, L.C.,
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Gocayne, J.D., Tabor, P., Williamson, A., Homsi, F.H.,
Dugan-Rocha, S.D., Sodergren, E.S., Hodgson, A.H., Chen, R.C.,
Ayele, M., Scott, G.S., Worley, K.W., Amamatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Beeson, K.Y., Brown, M., Buhay, C.,
Busam, D.A., Center, A., Chen, G., Chen, Z., Clerc-Blankenburg, K.,
Davenport, L.B., Dietz, S.M., Ding, Y., Dodson, K., Doup, L.B.,
Draper, H., Emery-Cohen, A., Ferriera, S., Garg, N.D.S., Houck, J.,
Hostin, D., Howland, T.J., Hume, J., Degwam, C., Jalali, M., Kovar, C.,
Liu, W., Mattei, B., McIntosh, T.C., Morgan, M., Moy, M., Murphy, B.,
Nelson, K.A., Ndassa, Y., Nguyen, N., Perez, L., Pittman, G.S., Puri, V.,
Scheeler, F., Shen, H., Strong, R., Tector, C., Wang, Q., Williams, S.M.,
Xiang, J., Zaveri, J.S., Zhou, J., Zorrilla, S., Sathh, H.O.,
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1 (bases 1 to 156526)
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AC010665.6 GI:20066019
HTG.
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Quality: Phrap Qualit:
Estimated Total Numbe
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
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REFERENCE AUTHORS

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Submitted (31-AUG-2001) Human Genome

TITLE JOURNAL

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Lewis I. L. L. J. Li. Z. Libharge O. Lieu C. Liu J. Liu M.
Malled H. Liczado, R. J. Liu K. Liuciar P. Luna, R.
Malled H. Liczado, R. J. Liu K. Liuciar P. Luna, R.
Malled H. Liczado, R. J. Liu K. Liuciar P. Luna, R.
Martinez E. Massey E. Machier, E. McLood M. P. Medodor, M.
Merinez E. Massey E. Machier, E. M. Micherson, E. McKenkow, S.
M. Worgan, M. Morris S. Moser, M. Neil D. Metson, J. Newtson, M.
Myuyen, A. Mguyen, N. Mgyen, N. Oyledo, R. Pece, A. Payton, B.
Pecery, J. Perez, L. Peters, L. Pickens, R. Primas, E. Pul. L.
Quilles, M. Ren, Y. Rives, M. Rojas, A. Roylubokan, I. Rolfe, M.
Ruilz, S. Savery, G. Scherer, S. Scott, G. Shen, H. Shoohkari, N.
Stoone, H. Sutton, A. Svack, A. Tabor, P. Theritod, B. Thomas, K.
Tangh, T. Tansey, J. Taylor, C. Taylor, T. Telfford, B. Thomas, N.
Tangh, S. J. Usmani, K. Jasquaz, L. Yera, V. Telladon, D. Vinson, R.
Malling, M. Martin, M. Maren, M. Martin, M. Martin, M. Malled, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin, M. Martin,
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Burch, P. Burkett, C. Burrell, K.L. Byrd, N.C. Carron, T.F. Carter, M., Gavazos, S.R., Chacko, J., Chavez, D., Chen, G., Cohen, R., Cher, S., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Davis, C., Edgar, D., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hernandez, J., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Martinez, E., Massey, E., Mawiney, E., McLeod, M., P., Meador, M., Marinez, E., Massey, E., Mawiney, E., McLeod, M., P., Meador, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Orghn, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Peters, L., Pickens, R., Primus, E., Pul, L., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Shooshtari, N., Stanley, H., Shooshtari, N., Stanley, H., Shooshtari, N., Stone, H., Shooshtari, N., Stone, J., Vinson, R., Walliamson, A., Washington, C., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Zorrilla, S., Nelson, D., Weitston, D., Vinson, R., Washington, C., Wu, Y., Wu, Y., E., Zonu, J., Zorrilla, S., Nelson, D., Direct, Submission
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REFERENCE AUTHORS REFERENCE JOURNAL TITLE AUTHORS JOURNAL Submitted (06-APR-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA 7 (bases 1 to 156526) Direct Submission
Submitted (03-FEB-2002) Human Genome Sequencing Center, Departing Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA Direct BCM-HGSC Direct Submission BCM-HGSC (bases 1 to 156526) Submission Center, Depar of Medicine, Department Department One

Submitted (01-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Apr 6, 2002 this sequence version replaced gi:15383763. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email

COMMENT

JOURNAL

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF TEATURES:
STSs are identified using ePCR (Genome of a local database that includes entries local mapping efforts. Res. 7:541-550) searches from dbSTS, GDB, and

source

/mol_type="genomic DN /db_xref="taxon:9606" organism="Homo sapiens' /mol_type="genomic DNA" Location/Qualifiers

15851

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the

EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

Matches Query Match Best Local Similarity 21; Conservative 0.9%; Score 21; 100.0%; Pred. No. 0, Mismatches DB 3; 28; 0 Length 156526; 0, Gaps

0

밁 100271 AAACCAAATTCTCAAATTGAG 100251 1508 AAACCAAATTCTCAAATTGAG 1528

REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION LOCUS DEFINITION RESULT 84 AL135926 COMMENT KEYWORDS TITLE JOURNAL requests: clonerequest@sanger.ac.uk

On Aug 14, 2000 this sequence version replaced gi:9621473.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure' Group. Further information can be tourned to http://www.sanger.ac.uk/HGP/Chrl
RP11-375F2 is from the library RPCI-11.2 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ IMPORTANT: This sequence is not the entire insert of clone RP11-375F2 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-375F2 is at 158519 in this The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Direct Submission Submitted (03-OCT-2000) Sanger Centre, Hinxton, Cambri CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AL135926 158519 bp DNA linear PRI 30-NOV-20 Human DNA sequence from clone #11-37552 on chromosome 1 Contains pseudogene similar to UBL1 (ubiquitin-like 1 (sentrin)), a pseudogene similar to ribosomal protein L29, ESTs, STSs and GSSs, Chapman,J AL135926.12 complete sequence. feature key. Homo sapiens Homo sapiens (human) GI:9801286 right of clone RP1-10C16 is at 100 in this Cambridgeshire, PRI 30-NOV-2000

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/note="L1MB5 repeat: matches 5460. .6168 of consensus"
6919. .7101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP11-375F2"
/clone_lib="RPCI-11.2"
460. .675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSx repeat: matches 1.
8551. .8624
 /note="L1M4 repeat: matches 3093. .3194 of consensus"
16839. .17215
                                                                                                                                  /note="MLT1E repeat: matches 385.
complement(14529. .15003)
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/note="AluY repeat: matches 214. .311 of consensus"
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/note="AluSq repeat: matches 12. .309 of consensus"
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note="25_copies 2 mer to
                               note="MIR repeat: matches 60. .153 of consensus" 6536. .16633
                                                                                                                                                                                                              3267. .13410
note="24 copies 6 mer tatata 78% conserved"
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                                                                                    note="match: GSS:
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                                                                                                                                                                                                                                            3254. .13403
note="75 copies 2 mer at 76% conserved"
                                                                                                                                                                                                                                                                                                                         3091. .13572
note="match: GSS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="L1PA8 repeat:
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                                                                                                                                                                       4045. .14226
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                                                                                                                                                                                                                                                                                        note="L2 repeat: matches 2576. .2669 of
                                                                                                                                                                                                                                                                                                                                                                           note="AluSx repeat: matches 1.
2419. .13151
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                                                                                                                                                                                                                                                                                                                                                         note="L2 repeat: matches 1683.
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                                                                                                e="match: GSS: Em:AQ798857"
1. .15366
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                                                                 .15463
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                                                                                  Em: AQ221861"
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                                                                                                                                                                    /evidence=not_experimental
complement(32129. .32630)
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/note="L1PA7 repeat:
19672. .20271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L1PA7 repeat: matches 5767.
17225. .17961
/note="L1PA3 repeat: matches 5410.
                                                                                                                                                                                                                                                                                                                               1722. .32025

'gene="bA375F2.1"

note="bA375F2.1 (similar to UBL1 (ubiquitin-like 1
                                                                 note="match: GSS: 3174. .33222
                                                                                                                                                                                                                                   atch: ESTs: Em:AI191222 Em:AI248769
atch: proteins: Tr:Q9PT08 Tr:Q23759 Sw:P55853 Tr:Q92172
w:Q93068 Sw:P55845 Sw:P55855 Sw:Q12306
r:Q97102 Tr:Q57686"
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note="AluY repeat: matches 1. .310 of consensus"
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1083. .22136
                                                                                                  omplement (32404.
                                                                                                                  note="match: GSS: Em:AQ093192"
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0761. .30877
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note="LIMC4 repeat: matches 6621. .7006 of consensus"
7982. .2815
note="LIMC4 repeat: matches 7094. .7422 of consensus"
8256. .28552
ROCE="LIMC5 repeat: matches 7262. .7589 of consensus"
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7347. .27437
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                                                                                                                                                                                                                                                                                                      atch: cDNAs: Em:U72722
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                                 .33725
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.31494
                                                 repeat: matches 2624.
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Score
21;
                                                                               Em:AQ195587"
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Length 158519;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on oct 21, 2001 this sequence version replaced gi:15022253. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all the particular to the overlap as described with a national sequence was finished as follows unless otherwise noted: all the particular to the overlap as described when the particular to the overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl
RP11-239E12 is from the library RPCI-11.1 constructed of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr: TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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ilarity 100.0%;
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/note="Sequence from uni-directional
terminator reads only,"
a 31711 c 32256 g 53507 t
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                        University,
On Feb 10, 2
                                                                                                                       Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6
                                                                                                                                                                                   Submitted (09-AUG-2001)
University, 4444 Forest
7 (bases 1 to 177385)
                                                                                                                                                                                                                                                                                               Submitted (11-FEB-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                          5 (bases 1 to 177385) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-FEB-2001) Genome Sequencing Center, Washing University School of Medicine, 4444 Forest Park Parkway,
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Direct Submission
Submitted (25-SEP-1999) Genome
University School of Medicine,
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2 (base
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Homo sapiens BAC clone RP11-368K23
AC010885
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Direct Submission
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Direct Submission
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Mammalia; Eutheria; Primates;
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Center project name: H_NH0368K23
              Contact: sapiens@watson.wustl.edu
                                                           Center: Washington University Genome Sequencing Center code: WUGSC
                                              Web site:
                                                                                          eb 10, 2001 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                            USA
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sapiens BAC clone RP11-368K23
                                                                                                                                                                                                   Department of Genetics, Park Avenue, St. Louis,
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dicine, 4444 Forest Park Parkway, St.
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >=

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30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The clone sequenced to the right is RP11-328L5, 200 bp overlap. Actual start of this clone is at base position 1 of RP11-368K23; actual end is at base position 24222 of RP11-328L5.

Location/Qualifiers
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NEIGHBORING SEQUENCE INFORMATION:
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                               rpt_family="L2"
7543. .17703
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AC104075.1 GI:17227277
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FI Homo sapiens (human)
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Waterston,R.H.
Direct Submission
Submitted (03-DEC-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: submissions@watson.wustl
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RESULT 88
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180643 bp DNA linear HTG 09-MAY-2002
MUS musculus chromosome UNK clone RP24-484F21, WORKING DRAFT
                    AC117257
AC117257.2 GI:20514968
                                                          SEQUENCE, 5 unordered pieces.
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  HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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78085. .83855
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51045. .54856
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24198. .26002
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/note="assembly_name:Contig14"
4907 . .6495
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Sequencing vector: plasmid; 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-MAY-2002) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA On May 9, 2002 this sequence version replaced gi:20069845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert size: 193000; agarose-fp
Insert size: 180243; sum-of-contigs
Quality coverage: 9.47 in Q20 bases; agarose-fp
Quality coverage: 10.41 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McPherson, J.D. and Waterston, R.H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (08-APR-2002) Genome Sequencing Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 180643) McPherson, J \cdot D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 180643) McPherson, J.D. and Wat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: M_BB0484F21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: submissions@watson.wust]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                          be preserved
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                                                                                                                                                                                                                                                                                                                               63633
63733
160535
160635
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17103
                                                                              /note="assembly_name:Contig10"
63733 . .160534
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160635. .162109
    'note="assembly_name:Contig7"
|62210. .171033
                                                                                                                                                                        'mol_type="genomic DNA"
'db_xref="taxon:10090"
                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                    clone="RP24-484F21"
                                                                                                                                                                                                                               .180643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Project Information
                                                                                                                                                                                                                                                                   2: contig of 63632 bp in length
2: gap of unknown length
4: contig of 96802 bp in length
4: gap of unknown length
9: contig of 1475 bp in length
9: gap of unknown length
9: gap of unknown length
3: gap of unknown length
3: gap of unknown length
3: contig of 8824 bp in length
3: contig of 9510 bp in length
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brown, A., Camarata, J., Campopiano, A., Chang, J., Chargo, J., Chapel, J., Colargelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., MacChan, C., MacChan, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., MacChan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Restti, M., Roya, A., Santos, R., Schauer, S., Schuber, S., Schauer, S., Schube, L., Sewery, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Direct Submission

N., Subramanian, M., Stophal Topting, M., Ye, W. J., Young, G., Submitted (2111M 2002) Whitchead Topting, M., E., M., Subramanian, N., Stophalaro, J., Nath, J., J., Marker, A., and Zody, M.
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                Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Deachunka R., Damesen, H., Paron, B., Peterson, K., Phunkhang, P., Pierre, N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (31-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC108815 181547 bp
Mus musculus clone RP23-239013,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Boguslavkiy,L., Boukhgalter,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 181547)
Birren, B., Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 181547)
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171134. .180643
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37481 c 38933 g 53097 t
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Lander, E.
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27;
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Rise, C., Rogov, P.,
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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 8, 2003 this sequence version replaced gi:28195423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rnis record will be updated with the finished sequence as soon as it is available and the accession number wibe preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert size: 1872000; agarose-fp
Insert size: 181147; sum-of-contigs
Quality coverage: 8.0 in Q20 bases; agarose-fp
Quality coverage: 7.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 (Consensus quality: 18070) bases at least Q30 (Consensus quality: 18094) bases at least Q30 (Consensus quality: 181059 bases at least Q20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center clone name: 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: L20929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
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15699
17444
17544
39809
39909
76851
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                                                                                                                                                                                                                                                                               15699.
                                                                                                                                                                                                                                                                                            vector_side:left"
                                                                                                                                                                                                                                                                                                                              clone_end:SP6
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                                                                         clone_end
                                                                                                                              76951. .181547
                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-239013"
                                                                                              note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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                       35684 c 36618 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39908: gap of 100 bp
76850: contig of 36942 bp in length
76950: gap of 100 bp
181547: contig of 104597 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15598: contig of 15598 bp in length
15698: gap of 100 bp
17443: contig of 1745 bp in length
17543: gap of 100 bp
39808: contig of 22265 bp in length
                                                                                                                                                                                                                                  .39808
                                                                                                                                                                                                                                                                                 .17443
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                            56407 t
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                            400 others
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REFERENCE
AUTHORS
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ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HS109M15/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113083 ACGAAGTTCGTATTGCTCAAT 113063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1539 ACGAAGTTCGTATTGCTCAAT 1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemistry: Dye-terminator-amersham: 47% of reads Chemistry: Dye-primer-amersham: 8% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 0 bases at least Q40 Consensus quality: 0 bases at least Q30 Consensus quality: 0 bases at least Q30 Consensus quality: 0 bases at least Q30 Estimated insert size: ##; agarose-fp estimation Estimated insert size: ##; agarose-fp estimation
Base score cutoff: 0.2; Minimal exon length: 3 bp > 'Repeats': BLASTN 2.0.14 (Altschul et al.)
Database(s): * RepBase: ALU (human), released 22-DEC-1995 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: ###;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-SBP-2000) GBF, Dept. of Genome Analysis, Mascheroder Weg 1, D-38124 Braunschweig, Germany, E-mail: info.genome@gbf.de On Feb 17, 2003 this sequence version replaced gi:15384820.
All annotations in this database entry are developed by computational tools. It is therefore not expeniently noted in the feature lines that evidence is not experimental.

Mapping was performed at The Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL513424 AL353775
AL513424.3 GI:28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Pr
1 (bases 1 to 184365)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HS109M15 184365 bp DNA linear Homo sapiens chromosome 9 BAC RP11-109M15, complete
                                                                                                                                                                                                                                                                                                                                                                             PROGRAMS AND PARAMETERS USED FOR ANNOTATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemistry: Dye-terminator-BigDye: 45% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center clone name: 109M15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://webace.sanger.ac.uk/cgi-bin/display?db=acedb9&grep=109M15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG.
                                                               & Skolnick)
                                                                                                                                                                                                                                                                                        + Analysis and annotation were performed with the automatic + first-pass' annotation and submission tool + 'AnnoMitter' (Hornischer & Bloecker).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scharfe, M., Conrad, A., Hornischer, K., Loehnert, T.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (cf. http://www.sanger.ac.uk/HGP/Chr9)
Mapping information is available via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bloecker, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                    Organism: human
Organism: human
GenScan (Burge & Karlin), Vers. 1.0
Used matrix: vertebrate; Minimum (
                                                                                                                                                                                                                                                 GeneFinder (Green), Vers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rect Submission
                                                                                                                         Organism: human
                                                                                Prior probability: 0.04; Overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                        (Zhang
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                                                                                                                                                                                                                                                                         Programs used by 'AnnoMitter':
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                084
                                                                                                                                                 Minimum score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
27
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                                                                                number: 0 > Xpound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                  (Thomas
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Minimum identity: 70 %;
> 'ESTs': BLASTN 2.0.14
Database(s): * embl
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RepBase: MIR2 (primate), released 22-DEC-1995 .
RepBase: THE (primate), released 22-DEC-1995 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STS database:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Using sequence with masked repeats
Minimum score: 60; Minimum identity: 70 %;
'Tandem Repeats': GDE 2.2 option 'tandem'
Minimum length 2 bp; Maximum length 20 bp; Score threshold 2
Treat N's as mismatches? YES; Allow uniform consensi? NO >
'Inverted Repeats': GDE 2.2 option 'inverted'
> 'Micro Satellites': GDE 2.2 option 'sputnik' (Abajian) > 'CpG
Islands': GDE 2.2 option 'cpg'
CpG island region size 100 bp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'tRNA Scan': tRNAscan-SE (Lowe & Eddy), Vers. 1.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * RepBase: L1 (primate), released 22-DEC-1995 RepBase: MIR (primate), released 22-DEC-1995 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   embl (EST, other), released -DEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum GC contents 50 %; Observed/Expected 0.6 > 'STS Scan':
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Margin: 50; Number of mismatches allowed: 0; Word size: 7
                                                                                                                                 /note="XPOUND prediction, score complement (3150 . .3200) /note="92% identity: matches 61. /rpt_family="THE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="91% identity: matches 62.
/rpt_family="THE"
114. .224
                                                                                                                                                                                                                                                                                                                                                                                         complement 2475. .2583)
/note="88% identity: matches 334. .442 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (2323. .2378)
/note="91% identity: matches 369. .424 of consensus"
                     /note="XPOUND prediction, complement(8738. .8890)
                                                                                                                                                                                                                                  /rpt_family="L1"
complement(2696.
                                                                                                                                                                                                                                                                                                                                                          /rpt_family="ALU"
2479. .2666
                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (2371. .2457)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="XPOUND prediction,
complement(1943. .1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment~clone_end:T7~vector_side:left
assembly_fragment~clone_end:SP6~vector_side:right"
                                                                                                                                                                                                                                                                                                                          2479. .2666
/note="MZEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (2006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="94% identity: matches 85.
/rpt_family="THE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DN
/db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="XPOUND prediction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
note="GENSCAN prediction,
                                                                                          'note="GA repeat"
                                                                                                                                                                                                                                                                              note="85% identity: matches 829. .924 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="86% identity: matches 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="XPOUND prediction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="RP11-109M15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * RepBase: THR ((human), released 22-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .184365
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                                                                                                                                                                                                                                                                                                                                                                                                                                               family="ALU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family="ALU"
                                                                                                                     .5901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                             prediction, score =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Altschul et al.) (EST, human), rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2017)
                                           score = 0.334"
                                                                                                                                                                                                          score = 0.274"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        score = 0.240"
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                                                            21;
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ilarity 100.0%; Pred. No.
Conservative 0: Michigan
                                                                                                                                                                                                                                /note="CA repeat"
complement(20400. .20508)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(13176. .13440)
/note="84% identity: matches 162.
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(12722. .12984)
/note="88% identity: matches 154.
/rpt_family="ALU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(15894. .15983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="IR1', 79% cv/rpt_type=INVERTED 13171. .13412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_
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12721. .13003
                                                                                                                                                                                                                                                                                                note="XPOUND prediction, score = 0.325"
19806. 19835
| note="homology = 93.3%, counts = 15"
| rpt_family="ac repeat"
                                                                                                                                                                                                                                                                                                                                                                /note="XPOUND prediction,
18859. .18883
                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(16156. .16224)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="84% identity: matches 71. .160 of
/rpt_family="THE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="XPOUND prediction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12709. .13002
/note="IR1, 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="TCTT repeat"
10724. .10894
                                                                                                                                                      'note="87% identity: matches 175.
'rpt_family="L1"
                                                                                                                                                                                                                    note="88% identity: matches 494.
                                                                                                                                                                                                                                                                                                                                                                                             note="XPOUND prediction, 18420. .18547
                                                                                                                                                                                                                                                                                                                                                                                                                                      note="GENSCAN prediction,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="90% identity: matches 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="TTTA repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="XPOUND prediction, 
12705. .12719
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l2302. .12394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="XPOUND prediction,
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                                                            0; Mismatches
                                                                                                                       prediction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79% complementary to IR1' (13162. .13453)"
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                                                                           DB 9;
27;
                                                                                                                         score = 0.739"
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                                                             JOURNAL
                                                                                                                                                                                                                                   Allen, C., Allen, H., Alsbrocks, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrocks, S., Amin, A., Anguiano, D., Allen, H., Alsbrocks, S., Amin, A., Anguiano, D., Allen, H., Alsbrocks, S., Amin, A., Anguiano, D., Allen, H., Alsbrocks, S., Amin, A., Anguiano, D., Allen, H., Alsbrocks, S., Amin, A., Anguiano, D., Allen, H., Alsbrocks, S., Amin, A., Anguiano, D., Allen, H., Alsbrocks, S., Allen, H., Alsbrocks, S., Allen, H., Alsbrocks, S., Allen, H., Barden, H., Bardwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Chen, C., Chu, J., Checko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacke, J., Charer, K., Cavacos, I., Ceasar, H., Cander, A., Chen, Z., Chu, J., Checko, J., Charley, M., Flagg, M., Durbin, K., Duval, B., Eaves, K., Daylado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Daylado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Daylado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Daylado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Daylado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Daylado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Hadden, S. L., Haddson, S. L., Hodgson, A., Hoster, M., Foster, P., Fernandez, S., Finley, Y., Havlak, P., Hadden, S. L., Hodgson, A., Hogues, M., Hernandez, S., Finley, S., Hulyk, S., Hulyk, S., Hume, J., Idebird, D., Jackson, A., Hogues, M., Hamilton, C., Hamilton, C., Hamilton, K., Hernandez, S., Liu, J., Liu, H., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, H., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu,
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Submitted (03-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                              Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus
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Submitted (19 NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23194715.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 (bases 1 to 188307)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 176131 bases at least Q40
Consensus quality: 178360 bases at least Q30
Consensus quality: 179208 bases at least Q30
Estimated insert size: 182713; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186945
187045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: GVTD Center clone name: CH230-373P11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor Co
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                                                                                                end sequence:BZ241333"
185598. .186478
/note="clone_boundary
clone_end:Sp6
                                                                                                                                                                                                                                                                                                                   /note="wgs_end_extension clone_end:T7" 14936. .15763
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clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
/mol_type="genomic DNA"
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/clone="CH230-373P11"
                     nd_sequence:BZ241334"
35575 c 34850 g 46244 t
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                           8245 others
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1592 ATTTTTGATGAACATGATATA 1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 191350; sum-of-contigs
Insert size: 180369; 6.9% error; agarose-fp
Quality coverage: 6.99x in Q20 bases; sum-of-contigs Quality
coverage: 7.42x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus quality: 190069 bases at least
Consensus quality: 190312 bases at least
Consensus quality: 190418 bases at least
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1 (bases 1 to 191750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: XGAP4; version 4.5 Chemistry: Dye-terminator; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                               be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will
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138077
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                                                                                          /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-148L4"
/note="assembly_fragment:00083
fragment_chain:1"
                                                                       /clone_lib="DanioKey"
                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                       57919: contig of 57919 bp in length 58019: gap of 100 bp 64419: contig of 6400 bp in length 64519: gap of 100 bp 79865: contig of 15346 bp in length 79965: gap of 100 bp 138076: contig of 58111 bp in length 138176: gap of 100 bp 191750: contig of 53574 bp in length.
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100.0%; Pred. No.
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7-148L4, *** SEQUENCING IN PROGRESS ***,
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27;
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NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
Submitted (22-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Ritagato, J. 15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 193,433 genomic DNA of 11g14 Published Only in DataBase (2000) Published Only in DataBase (2000) Published Only 10 DataBase (2000) Published Only 10 DataBase (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax:81-42-778-9924)
On May 30, 2000 this sequence version replaced gi:7328537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagaw
Japan (B-mail:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 193433)
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                                                                                                                                                                                  Quality coverage: 4.92x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: hattori@gc.riken.go.jr
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fragment_chain:2"
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60959: gap of 100 bp
72673: contig of 11714 bp in length
72773: gap of 100 bp
85821: contig of 13048 bp in length
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190127: contig of 1697 bp in 16
190227: gap of 100 bp
191605: contig of 1378 bp in 16
191705: gap of 100 bp
193433: contig of 1728 bp in 16
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178209: gap of 100 bp
181915: contig of 3706 bp in 1
182015: gap of 100 bp
18359: contig of 1581 bp in 1
183696: gap of 100 bp
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Submitted (12-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Dec 12, 2001 this sequence version replaced gi:16328262.
Draft Sequence Produced by DOE Joint Genome Institute
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Homo sapiens chromosome 5 clone CTD-2188H20, complete sequence.
ACU24569
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DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                    Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu Quality: Phrap Quality >=40 99.6% of Sequence; Estimated Total Number of Errors is 0.4.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                              /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2188H20"
a 36242 c 35229 g 58721
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190228. .191605
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                                                                                                                                                                                                                                                                      Location/Qualifiers
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100.0%; Pred. No.
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                                                                                Score 21;
Pred. No.
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                                                                 Gaps
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RESULT 95

	COMMENT	TITLE	REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL	AC114491 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS
Code: UWGCY Ce: http://www.genome.washington.edu uwgchtgs@u.washington.edu Center: SC Project Information project name: chr-1 clone name: RP11-270C12 (sc0661) Summary Statistics ry: Dye-terminator ET; 89% of reads ry: Dye-terminator ET; 89% of reads ry: Dye-terminator ET; 89% of reads ry: Dye-terminator ET; 89% of reads ry: Dye-terminator ET; 89% of reads ry: Dye-terminator Ed; Dye; 11% of re yrogram: Phrap; version 0.990319 us quality: 207698 bases at least 020 us quality: 207698 bases at least 020 us quality: 207698 bases at least 020 us quality: 207698 bases at least 020 size: 207698; sum-of-contigs coverage: 9.9x in 020 bases; sum-of- pequences: pequences: populy in progress 11-43646 AL513187, 2000-bp overlap 11-43646 AL513187, 2000-bp overlap 11-43646 Assessment: has been annotated with sequence qua computed by the Phrap assembly progra y edited bases have been reduced to vels above 40 are expected to have le 10,000 bp. se quality values are not generally values above 10,000 bp. se quality values are not generally values are available as p try's ASN.1 file. ce was finished as follows unless oth were either double-stranded or seque hemistry or covered by high quality at least one plasmid subclone or more nd the assembly was confirmed by rest lidation:	ိုင္ပင္ခဲ့ရ	02) Genome Center, University of W WA 98195, USA	698) .V., Zhou,Y., Phelps,K.A.,	Subm shed es 1 K., (K., (Subm ed (AC114491 AC114491 AC114491 AC114491 AC114491 AC114491 AC114491 AC114491.1 GI:19310310 HTG. HOmo sapiens (human) Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo. 1 (bases 1 to 207698) 1 (bases 1 to 207698) Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Buckley, D., Raymond, C. and Hauden, E. D.

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

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ACCESSION VERSION KEYWORDS	RESULT 96 AC119573 LOCUS DEFINITION	, dd	Matches	Query Match Best Local S																											
AC119573 AC119573. HTG; HTGS	24	9914 AACTGTTAL	21; Consei	atch sal Similarity	6476	2422	540			1553	1476	2447	2499	5752	1552	3734	2127	7431	2134	5483	1519	2912	1642	684	1153	845	8253	22641	4453	3000	557
3 GI:30017949 _PHASE2; HTGS_DRAFT.	s clone	AACTGTTAAAAATCTTGAAAG	rvative (0.9%; Similarity 100.0%;	6358	2381	<800	3365	<800	1511	1511	2506	2506	5747	1511	3660	2087	7350	2087	5369	1511	2878	1578	<800	1111	839	8138	22765	4397	3024	<800
9 3_DRAFT.	219687 bp RP23-75H23, WO	G 9934	Mismatch	core 21; Pred. No.																2375	4505	2551	3438	2535	11034	3005	6907	9793	4615	2673	1318
	DNA 1 WORKING DRAFT		0,	. 9	•												-			2554	4535	2554	3410	2554	10774	3018	6913	9578	4535	2720	1249
	linear HTG DRAFT SEQUENCE, !		Indels 0;	Length 207698;	6215	2246	15	}	3632	41	2097	716	632	1537	3208	3846	250		1 1	179	5094	10650	11091	2704	728	11097	331	16194	55.3	4827	11716
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			COMMENT	TITLE JOURNAL				Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,						AUTHORS	JOURNAL	TITLE					MCCETCHY, M., MCEWan, P., MCKETHAN, K., MELOXIM, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norman, C. W. (Coron, T., Coron, J., Nguyen, C., Nicol, R.,						AUTHORS	JOURNAL	AUTHORS		SOURCE ORGANISM

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KEYWORDS
SOURCE
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* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 44491 44490: contig of 44490 bp in length

* 44491 44590: gap of 100 bp

* 112691: contig of 68101 bp in length

* 112792 112791: gap of 100 bp

* 112792 112791: gap of 100 bp

* 112792 1149514: contig of 36723 bp in length

* 149615 206356: gap of 100 bp

* 149615 206355: gap of 100 bp

* 206356 210687: contig of 56741 bp in length

* 206456 219687: contig of 13332 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
21; Conserv
Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP Rattus norvegicus (Norway rat)
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149615. .206355
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44591. .112691
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/clone="RP23-75H23"
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밁 S

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

Center: Baylor Co

College

of Medicine

Contact: hgsc-help@bcm.tmc

Web site: http://www.hgsc.bcm.tmc.edu/

REFERENCE AUTHORS

JOURNAL

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rocus

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Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinb, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Engene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabhsi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerda, M., Houllon, S.L., Hodgson, A., Houge, J., Hodgson, A., Houge, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu,
                                                                            Submitted (113-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:23617936.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-caffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (26-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat Genome Sequencing Consortium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 223266)
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Genome Center
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REFERENCE
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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TE 1 (bases 1 to 226427)

RS Muzny, D. Marie ., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Biswalo, K., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, S., Chen, G., Coyle, M., Cree, A., D'Souza, L., Checko, J., Chavez, D., Chen, G., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fannander, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC106341
AC106341.5 GI:30581326
HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus clone CH230-154023, ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
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Consensus quality: 207235 bases at least Q40
Consensus quality: 209483 bases at least Q30
Consensus quality: 211150 bases at least Q20
Estimated insert size: 228805; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221314
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clone_end:T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Rattus norvegicus"
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44898 c 44784 g 57395 t 10816 others
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IN PROGRESS
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REFERENCE AUTHORS TITLE

JOURNAL

TITLE

JOURNAL

REFERENCE TITLE JOURNAL

AUTHORS

COMMENT

Center: Baylor Co Center code: BCM Web site: http://

College

of Medicine

Assembly program: Atlas 3.0;
Consensus quality: 211153 bases at least Q40

Center project name: GKSI Center clone name: CH230-154023

Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu ------ Project Information

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SOURCE

VERSION

COCUS

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Hernandez, Hines, S., Hladdun, S.L., Hodgson, A., Hogues, M.,
Jackson, L., Jacob, L., Jiang, H., Johnson, A., Hogues, M.,
Jackson, L., Jacob, L., Jiang, H., Johnson, R., Hogues, M.,
Karpathy, S., Kelly, S., Kally, S., Khan, Z., King, L., Kovar, C.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mandiney, S., McLeod, M.P., McNeill, T.Z., Mennen, E.,
Mayniney, S., McLeod, M.P., McNeill, T.Z., Mennen, E.,
Martiney, S., WcLeod, M.P., McNeill, T.Z., Mennen, E.,
Martiney, S., Wolson, P., McNeill, T.Z., Mennen, E.,
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Martiney, S., Wall, H., Perez, A., Perez, L., Pfannkoch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Plazor, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Shen, H.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Trabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Wang, J.,
Wang, O., Wang, S., Warren, J., Watek, A., Tabor, P., Taylor, C.,
Wang, O., Wang, S., Warren, R., Weix, White, F.,
Wung, D., Wallson, R., Wleczyk, R., Wooden, H., Worley, K.,
Willasana, D., Warght, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, J., Zhoo, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
                                                                        AL Submitted (13 MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:25007771.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bem.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
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Direct Submission
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VERSION
KEYWORDS
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AC112436
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Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyaeji, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, M., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gunaratne, P., Haaland, W., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, J., Haladun, S., L., Hodgson, A., Hogues, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Norway rat)
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Rattus norvegicus clone CH230-153L4, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC112436.5 GI:25006795
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NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 213655 bases at least Q30 Consensus quality: 215176 bases at least Q20 Estimated insert size: 223975; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.9%; Score 21; DB llarity 100.0%; Pred. No. 27 Conservative 0; Mismatches
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223249. .225286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="wgs_contig"
48875 c 48593 g
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/mol type="genomic DNA"
/db xref="taxon:10116"
/clone="CH230-154023"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236764 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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REFERENCE AUTHORS

JOURNAL

COMMENT

Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu Center: Baylor College of Medicine Center code: BCM JOURNAL REFERENCE

AUTHORS TITLE

JOURNAL

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SOURCE

ORIGIN

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Norgan, M., Norris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Pluzzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Svartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Warren, J., Warren, R., Wei, X., White, F., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yon, V., Yu, F., Zhang, J., Zhou, X., Zhao, S., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G., and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, XX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:22856698.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                 may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Rat Genome Sequencing Consortium.
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Lorensuhewa, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahhmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Mattinez, E.,
Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
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Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A. Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Leis, L., Li, Z., Liu, J., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Leis, L., Li, Z., Liu, J., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Leis, L., Leiz, Leiz, L., Lebow, H., Levan, J., Leis, L., Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz, Leiz,
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- Genome Center
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REFERENCE
AUTHORS
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AC130777/c
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
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Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Balden, D., Bardaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bladwin, D., Bandaranaike, D., Barber, M., Byrh, P., Brown, M., Belawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Claveland, C., Cockreil, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Dary-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draber, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Elgene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, B., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamilton, C., Hamilton, K., Harvey, V., Halland, W., Hamilton, C., Hamilton, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2127 CAGTAGAGGAAACACCTGCTG 2147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED RATTUS norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC130777.2 GI:23267876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus clone CH230-24M8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.h NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59222 a
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4988
233807
233907
235016
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231874. .233806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="wgs_contig"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="wgs_contig"
48477 c 48404 g
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/db_xref="taxon:10116"
/clone="CH230-153L4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Rattus norvegicus"
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4987: gap of unknown length
233806: contig of 228819 bp in length
233906: gap of unknown length
235915: contig of 1109 bp in length
235115: gap of unknown length
235115: gap of unknown length
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; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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, *** SEQUENCING IN PROGRESS ***,
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Hollins, B., Howells, S., Hulk, S., Hume, J., Idebird, D., Jackson, A., Jackson, L., Jackson, L., Jang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longado, R.J., Liu, Z., Liu, J., Louiseged, H., Lozado, R.J., Lux, Ma, J., Loues, J., Lorensuhewa, L., Louiseged, H., Lozado, R.J., Lux, Ma, J., Louiseged, H., Lozado, R.J., Lux, Ma, J., Loues, J., Lopez, J., Loues, J., Loues, J., Mandshawari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mahshawari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, R., Martin, R., Martinez, E., Mangum, B., Mapua, P., Manchenayor, J., Moore, S., Milosa, R., Montemayor, J., Moore, S., Mangum, R., Martin, R., Martinez, E., Montemayor, J., Moore, S., Mangum, R., Martin, R., Martinez, E., Montemayor, J., Moore, S., Mangum, R., Martin, R., Martin, R., Murphy, M., Nair, L., Mangum, M., Morris, S., Munidasa, M., Murphy, M., Nair, L., Mangum, M., Morris, S., Munidasa, M., Murphy, M., Nair, L., Mangum, M., Morris, S., Munidasa, M., Murphy, M., Nair, L., Mangeon, N., Norris, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., Pal, S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 22, 2002 this sequence version replaced gi:22218436. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (14-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 240929)
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Rat Genome Sequencing Consortium
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                               Center project name: GNZE
Center clone name: CH230-24M8
Center clone name: CH230-24M8
Center clone name: CH230-24M8
Center clone name: CH230-24M8
Center clone name: CH230-24M8
Consensus quality: 217337 bases at least Q40
Consensus quality: 220597 bases at least Q30
Consensus quality: 222697 bases at least Q20
Estimated insert size: 236179; sum-of-contige estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Baylor College of Medicine Center code: BCM
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TITLE JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

REFERENCE TITLE JOURNAL

AUTHORS

COMMENT

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces

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Search completed: November 14, 2003, 06:25:58 Job time: 8795 secs
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ORIGIN
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                                                                                                                                                      Query Match 0.9%; Score 21; DB 2; Length 240929; Best Local Similarity 100.0%; Pred. No. 27; Matches 21; Conservative 0; Mismatches 0; Indels 0
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/mol_type="genomic DNA"
/db xref="rtaxon:10116"
/clone="CH230-24M8"
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                                                                                                                                                                                                                                                         16895 others
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